SEQUENCE LISTING

<110> Zyskind, Judith
Ohlsen, Kari L.
Trawick, John
Forsyth, R. Allyn
Froelich, Jamie M.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard

<120> GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
ESCHERICHIA COLI

<130> ELITRA.031A

<160> 485

<170> FastSEQ for Windows Version 3.0

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aaaacgttta tattgtacct ttttgattaa ccattgggg   159

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gtcacctact caaacgttgga acgagcgat ttcgtttaga ccttctacg ccgtaatggt   140
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cgtccttccg agcgtaaaga gacactggt gatgtgacgc accgcattct gacagtgccg   300
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aacttcgata accagaaagg cgaatggccg aatggtctgc cctaatcgc attggcgnnt   540
ccttactan ccacttcctt cncttgtcc ccttatggca acacttaatt tattntaaan   601
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acgtaagcga atggagtggc cggaaaccto atagtgaccg cccaccagtt ggcctgcatc   180
ggtttgtagc gtacgcgggc catggcaat aagattcaga tactcagact cttccgggge   240
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ggtcaaatt gatgtttttt agtctgttgt caaagccgcn attatacccg taaccggcac   480
tacagcgca gtagaaaaga cccgacaata ctcctggcat gggcgttaaa gctcacagga   540
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attgagatcg ctatgaaata tcaacaactt ggaaaaatctt gnaaagcngg ttggaaaatg   660
gaaagtatc ggtcaagaag c   681

<211> 289
<212> DNA
<213> E. Coli

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tacttaagc agaacgatta agccttagga cgcttcacgc catacttgga acgagccgto   180
ttacggtctt taagcgcgga gcagtcaagc gcaccacgta cggtgtggta acgaacaccc   240
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atatggcacc cttttcact tttatatctg tgcggtttaa tgccgggcag atcacatcto   140
cgaggatttt agaatgtgtc aaattaccgc atccctggta aaagagctgc gtgagcgatc   240
tggcgacgc atgatggatt gcaaaaaagc actgactgaa gctaacggcg acatcgagto   300
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tgctgctgat gggtgatcca aaaccaaaat cgacggcaac tacggcatca ttctggaagt   420
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tgcgctggaa ggcgacgttc tgggttctta tcagcacggt gcgcgtatcg gccgttctgg   660

ttgctgctaa aagcgctgac gaagaactgg ttaaacacat cgttttgacc tttgttgcaa   720
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<213> E. Coli

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cttacagcg caaaaaggct ggtgactaaa aagtcaccag ccatcagcct gattcctcag   240
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ttctaccagg tctttagctt ctttcagacc caggccagtt gcg   475

<210> 7
<211> 149
<212> DNA
<213> E. Coli

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cagattttac caggtcttta gcttctttca gacccaggcc agttgcgcca cgtactgctt   120
tgataacagc aactttgtta gcgccagca   149

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<213> E. Coli

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ggacgtcctc tgcagtata ttaagtcgtc gatagaaaca agcattgaaa ggcacagcag   180
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agtcaccagc catcagcctg attcctcagg ctgcaaccgg aagggttggc ttatttaact   300
tcaacttcag cgccagcttc ttccagagct tttttcagtg atctgcgtc gtctttgctc   405
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aggccagttg cgccacgtac tgcttgata acagcaactt tgttagcgcc agcagcttc   480
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cgtccattac agacatagct gcaactgctt caatgatttt gatctttagt ggatagacat   660
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cttcaattc aggccagct tcttccagag cttttttag tgcttctgcg tgtctttgc   1?0
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tcagaattac gtcgaattca gttttttctt cagcagcttc aacgggcca gcagctacag   3?0
ctacagcc agcagcggaa acacgaatt tttcttccat tgcagagatc agttctacaa   4?0
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<0010> 10
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<0012> DNA
<0013> E. Coli

<400> 10
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ttgata   126

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<0012> DNA
<0013> E. Coli

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<0022> (11)...(262)
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tctaccagtt tttagcttc tttcagaccc aggccagttg cgccacgtac tgctttgata   1?0
acagcaactt tgttagcgcc agcagcttc agaattacgt cgaattcagt ttttttcttca   2?0
gcagcttcaa ccgggcagc ag   2?2

<0010> 12
<0011> 202
<0012> DNA
<0013> E. Coli

<0020>
<0021> misc_feature
<0022> (1)...(202)
<0023> n = A,T,C or G

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cggagagttc gcgcgcttgg attncgcaac gtcagccatt accgcagcgt cgtactgcag   1?0
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<0010> 13
<0011> 261
<0012> DNA

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gcaaacttct cgccatcaaa tagccctga ctggttagtt ttagcgcggg gatcactggc   180
agagaaagaa agccatctg aataaacggc tcatcgggta acggacgca ttcacgggcg   240
ggggtttca aggcgtaact t   261

<210> 14
<211> 204
<212> DNA
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ttttattat tatggggaag gtgttattta tgagtttcat ttatgccgta acgacaatga   120
actggggaat tagtataagc aggcgcgagaa taataatcat tgtgcaaatg ctaatttaat   180
taatactatt taaatattat ttgagcata tgcacataag gttg   204

<210> 15
<211> 242
<212> DNA
<213> E. Coli

<400> 15
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caatgaactc gggaattagt ataagcagcg cgagaataat aatcattgtg caaatgctaa   180
tttaatact attattttg agcatatgca cataaggttg gg   242

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<211> 212
<212> DNA
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tatgccgtaa cgacaatgaa ctggggaatt agtataagca gcgcgagaat aataatcatt   180
gtgcaaatgc taatttaatt aatactattt aa   212

<210> 17
<211> 433
<212> DNA
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cacagcaaca tgatgcctct gtacaacctt aacgtgcaac gggtgcaac aatggcaggg   240
atccttgcct acgcgaccag gacacgttg aaaaatcccg cgagcaaacc aagcagtaaa   300
gtgcgacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagcagc   360
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gtgcgccca ttg   433

<210> 13
<211> 658
<212> DNA
<213> E. Coli

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ctgcaacgct ctctgttatc aattttctgg tgacgtttgg cggtatcagt tttactccgt   180
gactgcttcg cgcccctttt taaagtgaat tttgtgatgt ggtgaatgcg gctgagcgca   240
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ggacgcgata atgaaaacgt tattaccaaa cgttaatacg tctgaaggtt gttttgaaat   420
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aaaaggatgt gtacaatgaa ttcagcattt gtgctgttc tgacagtttt tcttgtttc   600
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gaacgggagt tattaaataa aatatgcatt gtttcaatgc tggctcgttt acgtctgatg   360
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<212> DNA
<213> E. Coli

<400> 15
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ctgcctttc ttcgaataa gcagccatt agcgtcatag a   101

<210> 16
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<212> DNA
<213> E. Coli

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cgaggtgcag ttcgcccata ccgcgatga tggtctggtt agattcttcg tcagtccata   180
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cgatagcagc atggatgtcg cccgcgcgaa cttcttcgat ctcttcacgt ttgttagcgt   420
ggatctgaac gatacgacg aaacgctcac gtgcagcttt cacgg   465

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gaatacccat gttactacc gggtagcctg ccagcggacc tgctttcagc tgttcctgga   180
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gaccatactg aatacgacca ccagactgtt tcgcgtgttt agcttcaaca tcggtaactt   360
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gccnaacttc tttggaacnn tttacnggtt ggtaacngc cttttnaacn atcaacga   780
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cggggtnaac ccngnaaaa   858

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        <211> 349
        <212> DNA
        <213> E. Coli

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ctgcagcggg actgcttc agctgttcct ggatacctt atcaacggcc gggatgtatt   180
cgccaggat tacaccacc ttaatgtcgt tgatgaactc gtagcctttc gggtttgaac   240
ccggctccag ccagtacatg tcgataaaca   270

        <010> 24
        <211> 450
        <212> DNA
        <213> E. Coli

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ctgatcttc tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt   180
cggacgcacc tttaataact ataaataagt gtctgggcag atactatata aattaactta   240
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aatataatta atactctact tccagagtag   330

<210> 25
<211> 471
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(471)
<223> n = A,T,C or G

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atgactgatt gccgatacct gattaaacgg gtcatcaaaa tcatcattgc tgtttttacag   120
ctgatccttc tgtcttata acacaaggaa acgtacttaa ggtgccgtcc ggtgaaccag   180
tcggacgcac ctttaataac tataaataag tgtctgggca gatactatat aaattaactt   240
agtgaatgat tatgctaatg tcatcaatta aataaatata atggcgttaa ggcttcccag   300
taatataatt aatactctac ttccagagta gaatattaaa ttttatccgc gtggtgcatc   360
agcacaaatt tatcccacaa ctgttcttct gtctcgacat gccccccgat ctttnacaaa   420
tantattggg ggattnggcc cncccttttg ncaggctggg gtcntcctnat g   471

<210> 26
<211> 379
<212> DNA
<213> F. Coli

<220>
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<222> (1)...(379)
<223> n = A,T,C or G

<400> 26
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acaaggaaac gtacttaagg tgctgccggt gaaccagtcg gacgcacctt taataactat   180
aaataagtgt ctgggcagat actatataaa ttaacttagt gaatgattat gctaatgtca   240
tcaattaaat aaatataatg gcgttaaggc ttcccagtaa tataattaat actctacttc   300
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ttctttctgtc tcgacatgc   379

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<212> DNA
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aattagtta ttccaaatga ggaaaatctc ccggcgaaaa aacgggaga tgaaagtgtg   180
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taatccat gcctgccgga taagttgcgg cttaacgcca ggaagcgtgt cggccagttt   300
caaacctaata tctccgcagca gttttttcgc cggattggta ccggaaaaca gatcgcggaa   360
tcctgcata ccaggcagca tcaaccgccg actgtgcttg cggctacgct catcgcacg   420
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cagcctata cagattaaat cagaacgcag aagcggtctg ataaaacaga atttgcctgg   540
cggcagtagc gcggtggtcc cacctgacc catgccgaac tcagaagtga aacgccgta   600

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gcgcccgatg gtagtgtggg gtctccccat gggagagtag ggaactgcca ggcatcaaat    660
aaaacgaaag gctcagtcga aagactgggc ctttcggttt atctggtggt tgtcggtgaa    7.0
cgctctctga gtaggacaaa tccgccggga gcggattttg aacgttgcga aagaaccggc    7?0
ccggaaaacg gtgggggct                                                 7?3
```

        <211> 21
        <211> 636
        <211> DNA
        <213> E. Coli

        <220>
        <221> misc_feature
        <222> (1)...(636)
        <223> n = A,T,C or G

        <400> 21
```
aggggguttg tttgggcaa tgatgcattt aagttatcgt ctgcagatag aggagatatt     60
acaataaaaa agaatcagg gcatttgata gtcaatacgg caattctatc aggagatata    1.0
gtcactctaa gaggaggaga aattaggttg gtattatagc ttgtgcgcgc catgatgggc    1?0
gggcaatttg aattagttgc cttacatcgc tattgtcttg atttctttga attattttat    2?0
aaattaaaaa aagactgtt atgtataagc aaaggtcgaa cgaaaaatac attccaaata    3?0
aatgctgct taatatctta tatccttccc cgaaaaaatga cacataaaat tgagatattc    3?0
caaaaagtga tactacaaat aaagatgcct ttattttatt attttctaata aaaatagaag    4?0
caataaaaa tgtcaacaat gatataaatc taatgttttt aaatatattg tctttttatgt    4?0
tagtaatagt cgttagtatg tttgattctc catatattac gtgtagtttt ttatatacat    5?0
ggaaatattt ntgttttatac tgagagcatca caccatcatc aaatggaagt ttgaagatgg    6?0
tgcttgtttt ggtaacaat aaaaagagtg cattcg                              6?0
```

        <211> 22
        <211> 757
        <211> DNA
        <213> E. Coli

        <220>
        <221> misc_feature
        <222> (1)...(757)
        <223> n = A,T,C or G

        <400> 22
```
cagcgggtgt atttctagca tggttttta ttggcggcta tgctgcccg ggagcataaa     60
gatgaaaaaa ataacgatta ttatgatggg tgtggcgatt attgtcgtac tcggccactga    1?0
gctgggttga tcgtaacgtc acctctaaaa aatagcaaag gctgcctgtg tgcagccttt    1?0
gtggaatttta atcgttaact tttaatcttc ctgtagataa atagcacgac aatcgcacca    2?0
ataacgtcaa cacgaaagt gccaaaattg aagccatcga ctttaccaaa gccaaacagc    3?0
gtgtgkatct at cggccgac tacggcaccg actatcccca gcaggatagt cataaagaat    3?0
ccacctcaat cttaccigg catgatccac ttggcagaa tacggcaat aagcccaaaa    4?0
ataatctattg aaagaatgcc catgtttcc tcaattatct gttttgcatt agcgggttag    4?0
tcgctgataa aaagcatagc acaacatgg gagggcaaga ttgtgacga gcatcacgga    5?0
ggtttttttt gcgatggcgc agaaattgcg ccatcaacga tcagtgataa ttaccaacca    6?0
caaacataaa gttcgttttc cgtgtcataa gaaccgtacg ggattcacca gatctttat    6?0
cacttcaagc ctgcacttct ggcaccagca aagtcatcgg cgtctctggt tcataatcga    7?0
ccggaaacgc cattgctggt attggtgacn gtcacgg                            757
```

        <211> 23
        <211> 742
        <211> DNA
        <213> E. Coli
```

<210> 30

```
aattacagaa aaaggaggca atatcgggta aaggcattag ccgacgaat  acgtcgggct   60
acaaatattu ttgtgctgca ggtgttttag cgggttgttg atccacaggt tctaactgga   120
agaccacatc gacctgatca tgaaactgaa tagcggcctg ctcgtaagtt tcctgggcgg   180
acaccggcg  ggcatggct  ttcatcatcc ggaccattgg gctgggctga tagttcggaa   240
cattgttacg cacgctatat accggcccca gtttacgatg aaagccgttc gccagttcct   300
gggcctgatg aatcggcttg tcaatcgctg ccttacgcgc ttgtgcttta taggcatccg   360
ggtgcgcac  gcccagcgac acagaacgaa tt                                  392
```

<210> 31
<211> 351
<212> DNA
<213> E. Coli

<400> 31

```
ctatccttca tgaaacgcg  agcaaagata ggtgattacg tcatggtttt acagaaaatt   60
acagaaaaac gaggcaatat cgggtaaagg cattagccg  acgaatacgt cgggctacaa   120
atattattgt gctgcaggtg ttttagcggg ttgttgatcc acaggttcta actgaagac   180
cacatcgacc tgatcatcaa actgaatagc ggcctgctcg taagttcct  gggcggacac   240
cggcgcggca tcgtttttca tcatcgcac  cattgggctg ggctgatagt tggaaacatg   300
gtagcgcacg ctatatacg  gccccagttt acgatgaaag ccgttcgcac g            351
```

<210> 32
<211> 762
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(762)
<223> n = A,T,C or G

<400> 32

```
aattatgaaa cactgtctgg aatcgtctga atgacgggca cattttgcgag cacgcatcca   60
gtaataacac aggaaactat tttatctacg cgttagcgat agactgcttg catggcgaaa   120
ggaggtcaa  cgacgatttc aggggacgc  tgaaacggga aagcccctcc cgaggaaggg   180
gccatacata agcaaagggt catgatgaag ctactcatca tcgtggtgct cttagtcata   240
agctccccg  cttactaaga ctaccaggc  ggggggaaac ccgtctacc  ctcactcctg   300
aaagctatgc ttcacgataa gattgtcaat ccgcaggctt tgtagtctgc gatcctgcca   360
gcaaatattt tttgccagtc gttagccaat aatcacagag gaaactattt tattcagccg   420
ttacgatag  actgcttca  gggcgaaagg aggtaagccg atgattccag cgggacgctg   480
aaacggaaa  gccctcccg  gagaagaggg cttttaataa ggaaaggggtt atgatgaagc   540
acgtcatcac atggtgata  ctcttagtca ttagcttca  ggcttactaa gaacaccagg   600
gggaggggta aactcttcc  taacctcac  ttctgaatt  gggtgctatg acgctggcgt   660
tactgcttac cgctaccagt ttgtctgccc tggcggttgt aaagccagat cggtacccgt   720
ttggatattt taatgaaagc cgacaaatca atcaacgtga cg                      762
```

<210> 33
<211> 243
<212> DNA
<213> E. Coli

<400> 33

```
gcacatttgc gatcacgat  ccagtaataa cacaggaaac tattttatct acgcgttagc   60
gatagactgc ttccatggcg aaaggaggta agccgacgat ttcagcggga cgctgaaacg   120
ggaaagcccc tcccgaggaa ggggccataa ataaggaaag ggtcatgatg aagctactca   180
```

-10-

tcatcgtggt gctcttagtc ataagcttcc ccgcttacta agactaccag ggcgggggaa   240

acccccgctt accctcactc ctgaaagtat gccttcacga taagattgtc aat   293

        <210> 34
        <211> 633
        <212> DNA
        <213> E. Coli

        <220>
        <221> misc_feature
        <222> (1)...(633)
        <223> n = A,T,C or G

        <400> 34
atttacactt ttacgaaat catgggatca ctaacaaaat atgcttgtc agttatattg   60
tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca   120
ttaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tggccgcac   180
cagccaccc gggttcgacc aatacctcgg gaattctaa gtatgagtta agtagtttca   240
ttgctgatt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg   300
agtacaaat taagcagtgg cagttgcgta acctgcccgc gcctgatcc gggacgcact   360
ggacctatat ggtgggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag   420
cctacgcgg tgcgattttt tatcatcgct aaaaaaagcc cccctcatcat gagggggaaa   480
tgcagaaaan ttgntatttt ttattattag ccacttgctc gtcttgcttg gtattaagtc   540
gtatttcacn ttgattaatg cnggtggctc cagtgcgcca gattaacttt gtttggatcg   600
aagacgtagt aactggctgg ttatcggaat tgg   633

        <210> 35
        <211> 569
        <212> DNA
        <213> E. Coli

        <400> 35
tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca   60
ttaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tggccgcac   120
cagccaccc gggttcgacc aatacctcgg gaattctaa gtatgagtta agtagtttca   180
ttgctgatt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg   240
agtacaaat taagcagtgg cagttgcgta acctgcccgc gcctgatcc gggacgcact   300
ggacctatat ggtgggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag   360
cctacgcgg tgcgatttt tatcatcgct aaaaaaagcc cccctcatcat gagggggaaa   420
tgcagaaaan ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg   480
tatttcacn ttgattaatg ggttgcctac agtcgcag attaactttt gtttgtatcg   540
tagacgtagt aactggctgg tatcggaat   569

        <210> 36
        <211> 338
        <212> DNA
        <213> E. Coli

        <400> 36
cgtatttaan tccttttgat tggtgataac atgcgaatcg gtattatttt tccggttgta   60
atcttcattn cagcggtgt attttttagca tggtttttta ttgggcgcta tgctgcccg   120
ggagcatnn gatgaaaaaa acaacgatta ttatgatggg tgtggcgatt attgtcgtac   180
tggcanncn ctggatggt ggtaagtca cctctaaaaa ataccaaagg ctgcctgtgt   240
gcagccnnta tgcaatttaa gcgttaactt ttaatcttcc tgtagataaa tagcacgaca   300
atcgcanna taacggcaac cacgaagctg ccaaaatt   338

        <210> 37

<400> 37
```
ctgaatatt  aaaagaaa   acgacatgaa  acgaagcac   agaatcaaca  ttctccaatc   60
ataaatatt  ttcgtggag  attttattat  tgaatataga  ggtttaactc  cggtaaaaaa  120
caaagaagca  ttaatgcat  ggaaaaataa  tatggccata  aaaaacatcg  aaagaaactc  180
tttaatttta  acntgtaaac gcatggttaa  tcctcatatc  acgggtggag  tgttaagaac  240
atacataaat  ggagtcatgt tttccctttt  ccattatca   agttcctgtt  ggcgttttag  300
tccatcttta  attgcatatt ttaatttttc  tgataaatgg  cattgagcat  cgatttcatt  360
taaaacaact  gtaca                                                      375
```

<400> 38
```
ttacgatagc  tattagtaaa  aatataagag  ttagctgtat  tgttatgtct  gtgggaaat   60
tgactacctt  cgtttttttg  attaagaatg  attttattat  cgtaagtaaa  attacatgaa  120
tatttaaaaa  ggtaaacgac  atgaaaccga  agcacagaat  caacattctc  caatcataaa  180
atatttccgt  ggagcatttt  attattgaat  atagaggttt  aactccggta  aaaaacaaag  240
aagcattgaa  tgtagggaaa  aatataatgg  ccataaaaaa  catcgaaaga  aactctttta  300
atttaaaatg  tatacgcatg  gttaatcctc  atatcacggg  tggagtgtta  agaacataca  360
taaatggagt  catgtttttc  cttttccatt  tatcaagttc  ctgttgccgt  ttagtccat   420
ctctaatttc  atatttaat   ttttct                                         446
```

<400> 39
```
tcacccgtt  gcggattttc  aggcatcctg  atttaactta  gcaccgcaa   cttaactaca   60
ggaaaacaaa  gatataaatg  tctaatcctg  atgcaaatcg  agccgatttt  ttaatcttta  120
cggattttta  cggctggt    ttattaattg  cactgtatc   cgggcgttcg  ccggcttaa   180
tcacaatagg  ctgtagcc    tgggctgtt   tctctttcac  ccgcgccaga  gcggcagcaa  240
tcgcatcttt  atcttgggt   gcaggttgaa  cggctcgct   cttatgtcgt  tcaaggcgag  300
ccgttttc    gtctccaga   cgagcctggc  gcgctccgaa  agcgctttg   gcttctgcgg  360
cacgctttc   ttctgacga   atagccgaa   tt                                 392
```

<400> 40
```
taataacgct  atctgcggat  aaagcagaat  aggtggttaa  cccagacat   aaaccgagga   60
aaataatgtt  atcgtatttc  ataatctatt  gttccttagc  gacagattgc  tgtctgctgg  120
ttcagtaaag  taccaagaga  aacttcagga  agcttgtact  cgacaataca  gtttgagttt  180
ttatcttttg  cccatgaaac  ctgtaatt                                        208
```

<210> 41
<211> 242
<212> DNA
<213> E. Coli

<400> 41
catcctcaat accgttaaat gcaacccgaa cccccgttgt cccttttgctg cattcactta   60
acgtaatttg aaaagggacg gctggacttg tgctaccggt cgttggaaat tgtctggcac   120
tgtttttttg gagatctacg gtaaaattaa gcgaatccga tgagactgtg cagccataat   180
cgaggacgcg ccggctaatt ttaataacgc tatctgcgga aaaagcagaa taggtggtta   240
acccccacca taaaccgagg aaaaataatgt tattgtattt cataatctat tgttccttag   ---
cgacagattg ctgtctgctg gttcagtaag gtaccaggag aa   242

<210> 42
<211> 841
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(841)
<223> n = A,T,C or G

<400> 42
agatttactg ctaatttccg gcagatcgga aagggttaaa ccatattgat ccataagggt   61
acgaatcacg gctataccgc caggcatggc ttgagccatg gcattaaatt ccgcaaattc   120
gggcgctaat ctttccacg cggttatttt ggcacacacc agatccagca aggggtttctc   1:
aggatcgttt agcagcagat gatctaccag ttncagcgcc tgggtgtatt gntccttgtt   240
ctgaatacctc gtnagaaaag gtgccacagc anttagcttn tctcctgctt gcaagatgtc   3..
tggcaatcgc aatcattttt tgcacttant acgatgnaca ncngtaaaga aatcgnattt   300
ttntatnttt tcataactttt acgtatgtan cacttttgc nattcnaaaa aagaccattn   4..
gctncaacac gtaaatttna ttgncccna catttanaac ataaatgntt aaaattttcc   4
ccccncnnan ttttaagntn ttnanagaat nggaattac ctgcttttna atgnactcan   5..
antttttttq naataattcc tntatcnaan ctnntttton cccaanagnc nnccaaattn   600
cggtttntn ntnnnnnngg cntttttta cccnanaann tttattcaan ncctttttg   6..
tagnctattt naaqnqqnct ttntnnatt aactttccnn ttggncaaat tttggcnnat   7..
ttttatatan aattntctta tntcntaatt tnggnancc cngatgnaan tttatggngg   1..
gantccccnnt ccctntttaa tnnatgntct gggntatttt caaanccctnn attnannnan   640
c   641

<210> 43
<211> 215
<212> DNA
<213> E. Coli

<400> 43
aataacttct cgntaggcag ttttgggtgt gagttgcaag aggggagact actgaataac   60
tcaagtttta taatcgaggg gaaaatggtg atggcgttca tagcaaaacg ccctcaacca   120
taaaggtcga gnncgttaa gatgttaaaa accgctatc cgttaaaaaa caatgttcaa   180
ctaaggtcag tgacattgcg ctaaaaaagc gaatt   215

<210> 44
<211> 395
<212> DNA
<213> E. Coli

<400> 44
```
gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac catttgttat     60
ttaaggttta attatctgtg tgtgatattt tattgaatgt tttaaatatt gtttttattg    120
gcattgtat  aaatattggtt atcatttgct gaatggattc agtcttaatg agtgggtttt   180
taaggatag  gcatagagta atgatacgta tgcataacca acatctttac tcattatgtc    240
attgaatgtt gaccctatgt gtttatgaag gagaggtatt ttcagttgat ctggattgnt    300
aaattcatat aatgcgcctt tgctcatgaa tggatgccag tatgtagtgg gaaattataa    360
atattgaaat agtccaacta cttcctttatt accaa                              395
```

<400> 45
```
ataatcaggt aagaaaaggt gcgcggagat tacgtgtgt tgcgatatat ttttagttt      60
cgcgtgtaa  tatatcagtg gcaataaaac gacatatcca gaaaaatata cactaagtga    120
atgatatctt ccgattatc ttaatcgttt atggataacg gcaaagggct tcgttttttc     180
ctatacttat tcagcactca caaataaagg aacgccaatg aaaattatac tctgggctgt     240
attgattatt ttcctgattg ggctactggt ggtgactggc gtatttaaga tgatatttta    300
aaattaatta atgtcatcag gtccgaaaat aacgagaata tttcagtctc tcatcctgtt    360
gcgctcctgt catgtgcatt gcttcatata atactggcg caaggagcgc cgcaggcgna    4.0
gnntgcncgn cgncccacct naccccatgc cgaacttcag aantgaaaac nccntaacnc   480
cgatngtcgg cncgncctc cccatgcnan agtangggaa ntgccangcg ncnnattaaa    540
cgaaagnctn attncaaaga ctgggcctn cntttatctg atgtttgtcg gagaacgtc    600
tcctgacnan gacaaaatnc gccgggagcg gattgaacn ttgcgaagca acgncccna    660
agggngnngt cntgacnccc nnctanct nngccttc ttttgcttna angncctcct      720
ancngat    ctttngcc nctaccaaa cnntttggtt aatgcttnta aaanccttc       7.0
cannntn    tccngtnntn cccatccnn tnnngaaagn ntncctncn tgtncantnt      840
anntnn     gnncgngncc gggggnccc ccccccccc ccc                       883
```

<400> 46
```
gtttatggat aagggcaaag ggcttcgttt ttcctatac ttattcagca ctcacaaata    60
aaggaacgc  aatgaaaatt atactctggg ctgtattgat tattttcctg attgggctac   120
tggtggtga  tggcgtattt aagatgatat tttaaaaatta attaatgtca tcaggtccga   180
aaataacgag aatatttcag tctctcatcc tgttgcgctc ctgtcatgtg cattgcttca    240
tataatcact ggcgcaagga gcgcgcagag tnctccnant nnnnntnntt ntntnnctnn    300
```

nccttcacna trcnnccncn nantnnatag nncacnnntn ttnntcnnnn gnccncctcc   360
nnncnnnnnc ncatnnnatc ccactnnntt tnctccannn nnncnnnntn canccnacaa   4?0
antcncatcr. anntnacctt atacnnannc nancnnnnnn nnccactctn nctgnncto   460
ccnttcnac. nnncannnnn cancnntcnn ctnnnncct nnntaattn ttctnnctan   ?40
ntcctanrcr cnnacnnncc cancnatccn nnnatacant cnattrntnn cnntcncntn   600
cncnnttcc nnctnnncnc tncncatnc cnnannannan canntrccc ncctncctna   660
ccncncnnc cnccatccc nnnccnnct cnnantnga caannnnnaat cncnnnnncn   7?0
nannnncnn trnncccn gcncnnct ncctcncnc tnnncncta nannnnntac   7?0
nntnacrnt cctnncacnc tncctnnng antcnacna ntnnnnnnanc nanaacnctn   ?40
tnnnncata atccacacc acnccntnc ancntntnnt ncntcntccc ttcntatcnc   ?00
agctnnnnt nrtnnnnnc tncncnccnn cnnactncnn nnaccncncn ccantcagt   ?60
ccaccntccr. cnncnnnntn nnncnancan ctnncacncn cnantaacct nntnncacct   10?0
cccc   10?4

            <210> 4?
            <211> 236
            <212> DNA
            <213> E. Coli

            <400> 4?
atatacantca agtgaatgat atcttccgat ttatcttaat cgtttatgga taaaggcaaa   6?
gggcttcrtt tttcctata cttattcagc actcacaaat aaaggaacgc caatgaaaat   1?0
tatacctrrc grtgtattga ttatttcct gattgggcta ctgctggtga ctggcgtatt   1?0
taagatgata tttttaaaatt aattaatgtc atcaggtccg aaaataacga gaatat   ?36

            <210> 4?
            <211> 418
            <212> DNA
            <213> E. Coli

            <220>
            <221> misc_feature
            <222> (1)...(418)
            <223> n = A,T,C or G

            <400> 4?
cggagattac cgtgtgttgc gatatatttt ttagtttcgc gtggcaatac atcagtggca   6?
ataaaacgrc atatccagaa aaatatacac taagtgaatg atatcttccg attatctta   1?0
ntcgtttat g gataacggca aagggcttcg ttttttccta tacttattca gcactcacaa   1?0
ataaagraac gcaatgaaa attatactct gggctgtatt gattattttc ctgattgggc   ?40
tactggtgrt gactggcgta tttaagatga tatttttaaa ttaattaatg tcatcaggtc   300
cgaaaatacr gagaatattt cagtctctca tcctgttgcg ctcctgtcat gtgcattgct   3?0
tcatatactr actggcgcaa ggagcgcgca ngggcgggcc aatcgccgcc ggccctg   418

            <210> 4?
            <211> 550
            <212> DNA
            <213> E. Coli

            <400> 4?
ctgctagtta cagggaacac taatgacaga cagctaaaag cctgtttaa ttagtatta   ?0
caaacagtgg atgccagcg ttttcgtgca tttattggtg agatagcgga aggcgcacca   1?0
caagaaaagg agaaactgat gaccattgct gacagattac gtgaagaagg cgaatgcag   1?0
ggcaaacacg aagaagccgc gcgtattgct caggagatgc tggatagagg tttagacaga   ?40
gagttagtta tgatggtgac ccgactttca ccagacgatc ttatcgcgca aagccactaa   ?00
tcctgtacca cgggagttca actggcggat gtttgctgta aaccacatca ggaacgaca   3?0
tccgccagcg cctcttctaa atcgtaccag cgaaacgcaa aacccgcttc ttccagccgt   4?0

ttaggcagcg cggcttgtcc acctaatacc agtactgaag attcgcccat taacagtcga   480
atggcggtcg cggggacgcg caaaatggcc gggcgatgca gcgcatgacc gagcgcatgg   540
gcaaaattgt   550

    <210> 54
    <211> 99
    <212> DNA
    <213> E. Coli

    <400> 54
ttggcatctc ggtgctgccg atcttcatga tatccagccc gccggaaact tcttcccaaa   60
cggccttgct gctatccatt gagtcacgga actgcccct   99

    <210> 55
    <211> 259
    <212> DNA
    <213> E. Coli

    <220>
    <221> misc_feature
    <222> (1)...(259)
    <223> n = A,T,C or G

    <400> 55
ccgtgctta atatatctgt naccatcatc cgtcgtgaag cagtgattca cgacttcaag   60
gcgctttca aaagggtatt ttggctttga catattaggg gctattccat ttcatcgncc   120
aacaaan:gt gttcagtaca tactcnttgg aaaatcaacac aggaggctgg gaatgccgca   180
gaaatataga ttacttctt taaatagtgat ntgcttcacg cttttatttt cnaaanaagt   240
tnggcttact tctcgggnn   259

    <210> 56
    <211> 377
    <212> DNA
    <213> E. Coli

    <220>
    <221> misc_feature
    <222> (1)...(377)
    <223> n = A,T,C or G

    <400> 56
cagcagacg cggccttctt cgtcagattt cgcagtagtg gtaatggtaa tatccaaacc   60
acgaacgcc ttgactttat cgtagtcgat ttctgggaag atgatctgct caggacacc   120
catgctgtac ttaccacgac cgtcgaaaga cttagcggac aggccacgga agtcacggat   180
acgaggtaca gaatagtga tcaggcgctc aaagaactcc cacatgcgtt cggcacgcag   240
agttacttta cagcgatcg gatagcctg acggatttg aagcctgcaa cagattgcg   300
tgctttggta atagcggtt tttgaccgga gatgctgcc agtctgctg ctggttatc   360
cagcagttt ttgtcagcga tcgcttacc aacacccatg ttcagggtga tctttctgac   420
ccgagggat tgcatgacag aattgtagtt aaactcagtc atgagtttt taactactc   480
gtctttgtac taatcatgac gtttcgccat cgtactactc catgtcggtg aagctctcc   540
tgagtagcac aaaatcgccg ggagcggatt tgaacgttgc gaagcaacgg ccggagggt   600
ggcgggcagg acgcccgcca taaactgcca ggcatcaaat taagcagaag gccatcctga   660
cggatggct tttggcgttt ctacaaactc ttttggtcat tttttctaaat cattcaaata   720
tgtatccgnt catcccatcc tatcgatgat aagctgtcaa acatgagaat ttaatcaatc   780
taaagtttta tggngttaaa cttgggctgg cagnttncca atggcttaat cagtngaggg   840
ccctatntta acgaactngg ctantttngg tcaatcn   877

<210> 52
<211> 291
<212> DNA
<213> E. Coli

<400> 52
tgaacagcag agatacggcc agtgcggcca atgttttttg tcctttaaac ataacagagt   60
cctttaagga tatagaatag gggtatagct acgccagaat atcgtatttg attattgcta   120
gtttttagtt ttgcttaaaa atattgttag tcttattaaa tgcaaaacta aattattggt   180
atcatgaatt tgttgtatga tgaataaaat ataggggggt atagatagac gtcattttca   240
tagggtata aatgcgacta ccatgaagtt tttaattgaa agtattgggt t   291

<210> 54
<211> 282
<212> DNA
<213> E. Coli

<400> 54
ttattaaatc caaaactaaa ttattggtat catgaatttg ttgtatgatg aataaaatat   60
aggggggtat agatagacgt cattttcata gggtataaa tgcgactacc atgaagtttt   120
taattgaaa tattgggttg ctgataattc gagctgttct attccttta aatatctata   180
taggtctgtt aatggatttt attttacaa cttttgtgt ttaggcatac aaaaatcaac   240
ccgcccatatg aaggcgggt caaaatattt acaacttagc aa   282

<210> 55
<211> 333
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(293)
<223> n = A,T,C or G

<400> 55
cggggtcgg cgttcatcaa caatcggggg gcagcaaggg gctgaaacgg gaaagccct   60
ccgaataat gggcttgta taaggaaagg gttatgatga agctcgtcat catactggtt   120
gtgtngttat tgttaagtt ccgacttac taacaactca tcagagggg gagaaatcct   180
ccttatcct tgttccttta ctctaggttg aaaaaacaac agcgtcaata ggcctgccat   240
gtacgaagcc agatctgtga accgctttcc ggttagcctt tttatcctg ttg   293

<210> 56
<211> 300
<212> DNA
<213> E. Coli

<400> 56
tctggtttct gctaaaaggt gcaaatgctc aggacgttgc agcgtttgc gtgaccgctc   60
ggggaattca aaattgcctc tgggaaagca ttgcgcgggg tcggcgctc atcaacaatc   120
ggggggtagt aaaggctga aacgggaaag ccctcccga agaagggcc ttgtataagg   180
aaaggttat gatgaagctc gtcatcatac tggttgtgtt gttactgtta agtttccga   240
cttactaaca attcatcaga gggggagaa atcctcsstt acccttgttc ctttactcta   300

<210> 57
<211> 359
<212> DNA
<213> E. Coli

<210> 57

```
caacacaaga ggctgggaat gccgcagaaa tatagattac tttctttaat agtgatttgt    60
ttcaggttt tatttttac ctggatgata agagattcac tgtgtgaatt gcatattaaa   120
caggagaati atgagctggc ggcgtttta gcctgcaaat tgaaagagta agagtcttcg   180
gcgggaatt attcccgcct tacttacggc gttgcgcatt ctcattgcac ccaaatttat   240
tcttcacaaa aataataata gattttatta cgcgatcgat tatttattc ctgaaaacaa   300
ataaaaaat cccgcaaa tggcaggat cttagattct gtgcttttaa gcagagatt       360
```

<210> 58
<211> 700
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(700)
<223> n = A,T,C or G

<400> 58

```
aaaccttttt ctcctgtttt tcatagaggg caacccatgt cctgacctgg gttcgggggga    60
caccaaaag tgccgagatg atcctgtaac catcatcagt tgtgaagtag tgattcaaga   120
cttcaaggcg ctttcaaaa gggtatttg gcttgacat attaggggct attcccattc    180
atcgtcaac aaaatggtg cagtacatac tcgttggaaa tcaacacagg aggctgggaa   240
tgccgcagaa atatagatta cctttctttaa tagtgatttg tttcaagctt ttatttttca   300
cctggatgat aaagattca ctgtgtgaat tgcatattaa acaggagagt tatgagctgg   360
gggcgttttt agcctgcaaa ttgaaagagt aagagtcttc ggcgggaaat tattcccgcc   420
ttacttacgg cgttgcgcat tctcattgca cccaaattta ttcttcacaa aaataataat   480
agattttatt acgcgatcga ttatttattt cctgaaaaca aataanaaaa tccccgccaa   540
atggcaggaa tcttagattc tgtgctttta agcagagatt acaggctggt tacgttacca   600
gctgcgggtc cttaagcgcc ggttcgatg gtgaaggaca cttctgacc ttcgtccaga   660
gattgtaagc atcggtctgg atagccagaa aatgtccaac                         700
```

<210> 59
<211> 631
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 59

```
tggtggcatt ggttgctgga gagagaaaac cccgcacgt tgcaggtatg caactgacaa    60
caccacgggg gctaatcttg actctagacc actcaagaat agccgcgaaa cgttgtcatt   120
acaacacag cgtctatatg acgttcgaag agctgggtat ggcttctgg cctgatttag   180
cggctcggt catgctggc attcttgcca gtatgatgt gaactggctg aacaagcgga   240
agtaacattt catgcgggcg tcaggctgcc gtaatggaaa tttgccccg gaccaggccg   300
caggggtgaa actctgggc cttttttgtt cttactgggg gtaaggcacc cagtcgcggc   360
cgttcagcg aagtacggt ttatcctggt attgaataac tactgcattt gagttctcgg   420
agaccgttgc tgtttgtggc aaaccactgg tgagtttttt ccagtcaaca ttgtcttcgg   480
tgaaaatctt gcatcgaga acgcgaacca ccagatcgga gatagccagg aagctgctcg   540
gttgttcat gaaaatcgt gcccctgat gcggtgcctt catgccgaag aatttcaccc   600
caacgggaac gtngtgata gacgggcta g                                    631
```

<210> 60
```

<211> 648
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(648)
<223> n = A,T,C or G

<400> 60
ggctcaggcn tgctgattgt tttttgtgc aatggcccng tattagcgtc gttgctgtcg   60
atggagagaa tcataaacgt ggtgaatgat gattgttagc aaggaaaact gtcaaaaatc   120
ttcaaaaat ttgaggtata aggccggaat ggctccggcc agagggaagt taaccgcgaa   180
gctgttgttg cttgagggtc gttttaacca gacgccaggc gctccatacg ccaaaacgc   240
gtctggttca gtggaccagc atattaggat ggcgaatcgt ccagatcgcc atcacgctac   300
tgccaactag cgcccaggag cgcagactta gcagcatatt ccancgacga tcgtaagcgc   360
ctgttgtctc cagccattca cgacgactgg cggaaggnc cgcgnctgac caagttgnct   400
tttagnctca tncaanattan attnataaac gcagnannch ggtntgatta atcntatttn   480
gctccngtct ggtagttagc nncggnnngt ctcntcntna cccnnttcnn tttannttac   540
natnngtaan ttatntttnt nngtcthant tntcanttgn tactntaagt ntatncgnnn   600
atnntnnnan nnnncagnnc ntnttttta aatnnttnt nannonnc   648

<210> 61
<211> 737
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(737)
<223> n = A,T,C or G

<400> 61
tgctaanatc tttctcattg agatgaaaat taaggtaagc gaggaaacac accacaccat   60
aaacggagtc aaataatgct gggtaatatg aatgttttta tggccgtact gggaataatc   120
ttatttttng gtttctggc cgcgtatttc agccacaaat gggatgacta atgaacggag   180
ataatctctc actaaccgg cccttgtta cagttgtgta caaggggcct gattttatg   240
acggcgaaaa aaaaccgcca gtaaacgggc ggtgaatgct tgcatggata gattcgtgct   300
ttgctttac gtaaacaggc atttctgc actgataacg aatcgttgac acagtagcat   360
cagtttctc aatgaatgtt aaacggagct taaactcggt taatcacatt ttgttcgtca   400
ataaacattc acgattttct tccggtttgc ttacctcat acattgcccg gtccgctctt   460
ccaatgac catccagagg ctcttcagga aatgcgcgac tcacacctgc tgtcacggta   540
atgttgtnt gtcttcaga atgtgtgatg ggatggttat cgactaactg gcaaattctg   600
acacctguc gaaatgctt ttcatcatta gcggctttga caataatgat aaattcttcg   660
cccgctat gataaacgc ttcgtaatna cgcgtccaac tgggntaagt aaagttgcca   720
gggtgccta atnttac   737

<210> 62
<211> 648
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(648)
<223> n = A,T,C or G

```
tgctttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca      60
aaaaccgata atctgaaaga acccaagtat ttcagtataa gcattgaatg ccgaccagta     120
aactcttbca gtttagccca gaaaagtgaan ccaaaatgat aatcgtatac ataagtcttt     180
cgagtgcctg gttagcaaaa agtttcaaca atggagtaaa tacatccaac atatcaataa     240
ctctcaactg taagggatt gaaatggtaa ccccagctct tcgcttgagg ggtatagccg       300
agaccaccga atcccccggag gtggtgaaat aaaaccgggc acaacacgaa agggcgcatt     360
tccgatatac ataaaagaag tcgggtcttt gtctggtaaa attaaattgg tgggaagtgc      420
ggctccgttt cttaaatacg gactttgctg ggtgtagtcc gggggcatca agtttttttc      480
tggaagttcg ctgatgtccg cccttttaa aggaattt ggtgatgccg gtgaatgccg         540
cttaacttta cgtgggccca gttaaaagtc atggtaagnc ctaatnggtt tggggtggga     600
aaagcchact gtnaattggt tacctggttt gcaagtancc ctggaagg                  646
```

```
ggtgttann tgaagagat tcatctttgt ntaaancccn gataagtaat tacgcataaa        60
acaacaaga ttataatagc aaaaataaat attatcatct ttgatagatt acttgagata     120
gcagcatat tgtaaaggcc ttatcgtttt tttatgctct ggattaatat aatcactaca      180
tctatctaag caatctgttg ttgatggaca tgtcaaccca tggtcattta cagccaa        237
```

```
gataatttana gtttgtcgtc agaaaattga cgttacccat aacaaatgaa aggccaggta       60
aatcatccca ttagtcatty ttgctatcgg tgtaatcttg ttgttgctcc tgatgatccg     120
cttaaaatcg acccggcttca tcgctctcgt cctcgtggcg cttgctgttg gattaatgca    180
aggaatcccg ctcgataaag ttattggctc catcaaagcc ggtgtcggcg ggacgctcgg     240
tagccttgcc ctcatcatgg gttttggcgc aatgctcggc aaaatgctgg cagactcggg     300
tggcgcacaa cctatcgcca ccacgctgat tgccaaattt ggtaaaaaac acatccagtc     360
gggcgtcgta ctcacggtt ttaccttcag tttttgcctg ttctctatgaag tgggctttgt   420
gctgatc                                                               427
```

```
caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga       60
aattaatgca attatcgaaa attcaaaaaa tatccaaaaa tngtatactt tattccagaa      120
```

```
gagttcaata taatgtttgt cttcaatttt tcttacttca gggtaatata gattgctcat      180
tacattgtga gcttcatctt tatttaattt tctgttgact ccagctctc gtgataacgg       240
ttttataatt agatgcttat c                                                261


        <210> 65
        <211> 98
        <212> DNA
        <213> E. Coli

        <400> 65
agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcacc ttacctgct       60
cttacgtac ttctgcgttg atagtaaaca tttctttc                               98


        <210> 67
        <211> 260
        <212> DNA
        <213> E. Coli

        <400> 67
aagcgcgaac gaagtcgatg tgctgcagct tcggtttgta cgggtgacgc tgtacgtcct      60
gagcttaac cttgattct ttacgtcaa caacgatggt cagaacttcg ctgtagaatt       120
cagcttacc ttcatgttc atgactttgt cgtgatccag ctcgatagc agcggcgctt       180
cttgcacc gtagatgatt gcgggaact tgttagcggc acgcaggcgg cggctcgcac       240
cctacctg ct tttacgt                                                    260


        <210> 68
        <211> 98
        <212> DNA
        <213> E. Coli

        <400> 68
aaaaacgggcg taaagaaagg ttgcaaacat gttaataaaa actcaaattg atcccacgta      60
tatattacgc cgcaaaatcc ttacaataaa caggg                                 95


        <210> 69
        <211> 174
        <212> DNA
        <213> E. Coli

        <400> 69
ttaattatta aaatagtgta acgcgattat gtggttatgg gggtaaacat taaataaacc      60
acgggaagg ggtggtaaag tgaaaaaata aaaagcggat aatcttaata agcaggcgg       120
acaacatcgc cat cggcac tgatacgagg tttatttcag ctcatcaacc atcg            174


        <210> 70
        <211> 138
        <212> DNA
        <213> E. Coli

        <400> 7
agtctgtaaa aacgtcaaaa agagtgtttt atcaacagaa gaatggaggt ctgacagata      60
gtagtactgt aacaaaatgg agacttaagt tgaatgaacg ggagtaaagc gaaaagacta     120
tagagtcaac gacaaatt                                                    138


        <210> 71
        <211> 141
        <212> DNA
```

<213> E. Coli

<400> 71
tttgttgggn taatattcta ttgttatctt tatttataga tgtttatatt gcatgaggtg   60
gttttttgga agaagaatga ggaagatgcg tcgagccaca gaaacgttag ctttacatat   120
agcggaggt atgtgaattt aatttacaat agaaataatt tacatatcaa acagttagat   180
gctttttgtn g   181

<210> 72
<211> 244
<212> DNA
<213> E. Coli

<400> 72
ggccatttat acaggaaaag cctatgtcag aaagtaaaaa ctcaaaatca cggccgtaatt   60
atctcgttaa atgttcctgc ccaaactgca cccaagagtc agaacacagt ttttcaagag   120
tacaaaaagg tgccctttg atctgccctc attgcaacaa agtattccag acaaatctta   180
aagctgtagn ctgattgatt ttattagtaa caagtatttt ttatatttta ataatatatt   240
taaa   244

<210> 73
<211> 3.7
<212> DNA
<213> E. Coli

<218>
<221> misc_feature
<222> (1)...(327)
<223> n = A,T,C or G

<400> 73
aaattttaaa gtacccttgtc accatactt tttttctgag cattaatgat attttgagct   60
tcttgaaaat cttaacctc ccacattggg tggaaagtat tcatatattaaa aggaaggntg   120
aataattrn cttataaaa cgccagtgga gaattagtaa aaacgattaaa ttctactaaa   180
tnattaaaca nanaaaaatt cccatatata tttatcattg gtatgaaaaa tatgtgcacc   240
atatttatga atntggatac cctnacagtc ctctgtgac gcatttcac cgatatgatt   300
tctttctna atcactaaaa cttttttt   327

<210> 74
<211> 150
<212> DNA
<213> E. Coli

<400> 74
gcaagtgancn aaacgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga   60
tgacttcnc cggagtcag gcggccactt cggtgcggtt acgtccgget ttctttgctt   120
tgtaaagnnc caaatctgcc gatttcaacc   150

<210> 75
<211> 330
<212> DNA
<213> E. Coli

<400> 75
gaaagtatct tcttattga catcactgga aaatataact tgcttttcat tattaaactc   60
gaagcgcgta ccttatctgg acaaacattt atcgagctta ccaaattcct gaagaggttt   120
aactacagat aacatttgcg cgtcctttgc agtaatgccc gtcaaatcct tgacgggcat   180

```
tatttaqutt aaattaccag tatttcttcg gagtgaagaa tattaccagg tatatttaac    240
acccacqttc gcggaccagt cttgatctac gtcaccacca ccgaggtagt tagcatcggt    300
ataggcqctg aagttcttgg tgaagctaaa                                      330
```

        <210> 76
        <211> 144
        <212> DNA
        <213> E. Coli

        <400> 76
```
tgtttttttc caqcacgga gcaaaaggtt tgccttgtg cagctcaggg ttaaccactt       60
taactacqtq gcgacgacc ggagatgtcg gcttacatt aacaactgcc attgtattac      120
tcctccaact tactcagcgc cgccaacgaa gtccagattc tggccttctt tcagggtgac     180
gtaagctttt tttc                                                      194
```

        <210> 77
        <211> 168
        <212> DNA
        <213> E. Coli

        <400> 77
```
tcccttaact tacccagggtg ttaacgactt cgacttcgac ttcaaacagt ttctgcacag     60
cagcttcat ttctgcttg gtcgcgtctt tagcaacttt gagtactatg gtgttggatt      120
ttcca ngt agcagacgct ctttcagaaa cgtgcggtgc acgcagcacc ttcagcagac      180
gtttcttca                                                            194
```

        <210> 78
        <211> 173
        <212> DNA
        <213> E. Coli

        <400> 78
```
acaaaggtga acaaagcctg tgaagcccga aggctccaca gacagtgcta cttgaaggcc      60
ttactgttt ttcttaggag cgagcaccat gatcatctgg cggccttcga tcttggttgg      120
gaaggat cc accactgcca gttcttgcaa atcgtctttc acgcgattaa gca            173
```

        <210> 79
        <211> 272
        <212> DNA
        <213> E. Coli

        <220>
        <221> misc_feature
        <222> (1)...(272)
        <223> n = A,T,C or G

        <400>   79
```
tggagaaaac ggctgattga taaagcaatc atcgttctag gggcgttaat tgcgctgctg      60
gaactgatcc cgcttttctgc ttcaagcttc tgaactggat acggaaacgt aatnagggct   120
aaagaaqcca ctactcttag cgcctttaaca tttaacgcat tgtcacgaac tcttctgccg   180
ccgttggttq aatgggacg ggtattggtc gaaatctttt ttgggtggcc ccatctttaa     240
cgcccatccq cgaaacctg caaacatttcg tc                                   272
```

        <210> 80
        <211> 259
        <212> DNA
        <213> E. Coli

<400> 85

cgcaggtagc tgatggtcaa caggatgaga gaaacccaga gacaggttaa tcacattgcc 60
tttaacgct gaaggtaac ctacaccaac cagctgcagc ttcttagtga agccttcggt 120
aacacctata accattgagt tcagcagggc acgcgcggta ccagcctgtg cccaaccgtc 180
tgcgtaccca ttaacgggac cgaaggtcag ggtattatct gcatgtttaa cttcaacagc 240
atcgttgaga gtacgagtc 259

<210> 81
<211> 7?
<212> DNA
<213> E. Coli

<400> 83

caggtcggaa cttaccgac aaggaatttc gctaccttag gaccgttata gttacggccg 60
ccgtttacct ggt 7?

<210> 82
<211> 666
<212> DNA
<213> E. Coli

<400> 82

atgaacgttt tctggaaac tcaacgctat aaggcgttgt tctggttatc gttatttcat 60
ctgtgttga ttacctccag taactatctg gttcagcttc ccgtctccat tttgggtttt 120
catacccatt gggcggcttc tagctttccg ttattttttc ttgctaccga cctgaccgtg 180
cgtatttttt ggtcacgct ggccgagc attatcttcg cggtaatgat ccctgcgtta 240
ttaatctct aatcatcc gtcgctattc tatatgggct cctggcaggg attgggcgca 300
ctggccaatc ttaactgct tgtcggcccgt atggccacgg ccagtttcat ggcctaggcg 360
ctgggtaaag tcgacgt gcagtttttt aaacgcctgc gtcagagtcg ccgctggtgg 420
ctggcattga catcgtccag actgttcggt aacgtcagcg acacgctggc cttttttct 480
attgccttct ggcgtacccc ggatgccttt atggctgaac actggatgga aatgcggctg 540
gtcgattact gttccaagt gttaatcagt atcgtttct tcctgccaat gtatggcgta 600
ttactccata tgctgttgaa aagactggca gataaatccg aaatcaacgc tttgcaggcg 660
agttaa 666

<210> 83
<211> 612
<212> DNA
<213> E. Coli

<400> 83

gtgataacat ggatgaatga gccgttatgg ccgtttatcg aaaggaagaa gtcaatgcgc 60
aatctgttta aatatgtcgg aatggcctg ctggttatgg ggcttggggc ctgtgatgat 120
aaagacctta atctaccggc gcaggttcg gtcgcggaaa gtaacgctac cgggaatccc 180
gtcgaaccgt ttatggaa gttaagtttc tcgctgccag cggatatgac cgaccagagc 240
ggtaagtcgt ggacgcaggc caataacatc catgtctggc ccgacgcac cgggcagaaa 300
gcagtcatct ctatcatggg cgatgatccg aaagaagatc tggcggtgct ggcgaagcg 360
ctggaagtca gtaacgtag ccgcgatccg cagctgcaag tggtaaccaa taaagccatt 420
gagctgaaag gtacaaaat gcagcagtta gacagtatta tctccgcgaa aggccagacg 480
ggtactcct ccttattct gggtaacgtg ggtaatcaac tgctgaccat gcaaattacg 540
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<211> 975
<212> DNA

<213> E. Coli

<400> 84

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<211> 1761
<212> DNA
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<400> 85

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<211> 1185
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<213> E. Coli

<400> 96
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<211> 540
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<212> DNA
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    <213> E. Coli

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<211> 885
<212> DNA
<213> E. Coli

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<210> 108
<211> 654
<212> DNA
<213> E. Coli

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caatggttga cgaaaacctt cggtacgccg cagatgggac ggatttgca ccggttcttc   180
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<210> 109
<211> 261
<212> DNA
<213> E. Coli

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tgcgtaggcg actacgagac accaacctgc cagaaggtgt gcccgatccc caatactatt   180
gtgaaagtc cgcgcatgt cgagacagaa gaacagttgt gggataaatt tgtgctgatg   240
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<210> 110
<211> 1203
<212> DNA
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<210> 111
<211> 1179
<212> DNA
<213> E. Coli

<400> 111

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<210> 112
<211> 1326
<212> DNA
<213> E. Coli

<400> 112

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tgcattctgc actcacacga aaacgagtgt gaaatcgccg acggcgacct gggtgttgatt   780
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        <210> 113
        <211> 5-5
        <212> DNA
        <213> E. Coli

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aacatttcgc aagtgggttta cgacgaagac gaagatcagg aagagcttga aatgtcgctt   480
gaagagatca tcgaatacgt tcgtgttgcc gcgctgttta tgccagacac ctttactcat   540
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        <210> 114
        <211> 363
        <212> DNA
        <213> E. Coli

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ggtttcgtca tctctgtgag ctttagcttc ttcgcgaatg caaaattcac attcaaggca   180
tcgactacaa cgctgcatta catgctatat gttgggttca tggggacact ggagtgctact   240
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gccatcagct tgttgtgcgg ttttgtctat tcaaagttca ttgtctttag ggatggcgaaa   360
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        <210> 115
        <211> 351
        <212> DNA

                                        -38-

<213> E. Coli

<400> 115
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gacggcagca aagacgctac ggagtcaatc attaatgctc tggctgtttc agatcctcta     180
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ggagatacaa aatttaatgg atggaaactt tggaatttag cacttgaggg tattacaagc     660
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<210> 116
<211> 1352
<212> DNA
<213> E. Coli

<400> 116
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<210> 117
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<212> DNA
<213> E. Coli

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ggcagcttcg tggttgccgt tattggtgcg attgtcgtgc tattatctca caggaagatt   260
aaaagttaa   249

        <210> 118
        <211> 147
        <212> DNA
        <213> E. Coli

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gatctgatga atccgtacg ttcttatgac acggaaaacg aacatgatgt tcgtggttgg   180
taa   183

        <210> 119
        <211> 360
        <212> DNA
        <213> E. Coli

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        <210> 120
        <211> 741
        <212> DNA
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cagtttgat attaggttga tgtggtcttc cagttagaac ctgtggatca agaacccgct   720
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-40-

acgtttcagg aagagaaact cttaacgatg aaaggtagtt ataaatcccg ttgggtaatc   180
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      <211> 132
      <211> 3123
      <212> DNA
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<210> 1__
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<211> 636
<212> DNA
<213> E. Coli

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<210> 137
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-48-

<210> 504
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<213> E. Coli

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<213> E. Coli

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<211> 315
<212> DNA
<213> E. Coli

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<210> 142
<211> 7152
<212> DNA
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ccaacaacgg cggaacttaa cgcctggctg aataattct ataacgcgga ggcgaaacgt   660
aaatgacct tccgtctctt gctgccgct gatgctcagc cattgacct actggtgatt   720
aacatctgtt cggtttcctg gtgggatata gaagcgcgcc ggttgatgtc gcatccactg   780
tggtcgcatt tcgatattga gttcaagaac tttaactccg ccacctccta cagtggcccg   840
ggggcgatcc gtttactgcg cgcagctgc gggcagactt cgcacactaa tctgcatcaa   900
ccggcaaata acgactgcta tctgtttgat aacctttcga aactgggctt tacccagcac   960

                                  -62-

ctgatgatgg gacataacgg ccagttcggc ggtttttttga aagaagttcg cgaaaatggc 1020
ggcatgcaga gcgaattgat ggatcaaaca aatctgccgg ttattttgct gggctttgat 1080
ggttcgccgg tttatgacga taccgctgtg cttaaccgct ggctggacgt taccgaaaaa 1140
gataaaaaca gccgtagttgc cacgttctac aacacggttc cactgcatga cggcaaccat 1200
tatccggggg tcagcaaaac agcggattac aaagcgcggg cgcagaaatt cttgatgaa 1260
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gtggttcgcg tttccgatgg caagattttc accgaagaca atgttgactg gaaaaaactc 1560
accagtgggt tgttacaaaa agcacaggtc tccgagaaact caaatgcagt agttattcaa 1620
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        <211> 304
        <212> DNA
        <213> E. Coli

        <400> 172
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gccggtagtt atgccactac cctgtgtcag gaaaaggagc aaaaatatcct taaggagatc 100
agctatcccc aaaaaacca aaaaccagaat cgtattgacg gtctgaataa agccctgagt 180
gaagtccggg ctaactgttc agatagccag ctgcgtgcca atcatcagaa gaaaatcgca 240
aagcagaaag atcaggtggc ggaacgccag caagatttag ccgaggcgaa ggaaaaaggc 300
gatgccrata agattgccaa acggaacgg aaactggaca aagcgcagga agagctgaaa 300
aagctgaaag cgtcgacta ctaa 304

        <210> 173
        <211> 306
        <212> DNA
        <213> E. Coli

        <400> 173
atgtcgaaag aacacactac ggaaacatctg cgtgctgagt tgaaaatccct ttccgatacg 60
ctggaagtgg tgttagctc atcggcgag aagtcgaaag aagagttgag taagattgt 120
agcaaagtgt agtaggcact gaaacagagc cgttatgcc tgggtgaaac cggtgatgcc 180
attgccaaat aaaatccgtgt cgggggcgcg cgtgccgatg agtatgtgcg cgaaaatccg 240
tggacggtcct tgtttcattgg cgctgcaatc ggtgtagttgc tcgggtgttct gctgtcgcgt 300
cgttaa 306

        <210> 174
        <211> 405
        <212> DNA
        <213> E. Coli

        <400> 174
atggcgtaca ctcatcaacgc acaaggggcc ggtaaaagcg tttctggcat cgggcagcga 60
atggttctta ccatggtcga aatggtagag acacgtctgc ggctggcggt ggtggagctg 120
gaagaggaaa aagcgaatct ctttcaactt ttactgatgc tgggcctgac gatgctttto 180
gctgcatctg gctcatgag cctgatggtc ctaattattt ggggcggttga cccgcaatat 240
cgcctgaatc cgatgatgc caccacgtc gtgttgctgc tactggcaact gattggcggt 300
atctggaggt actctaaatc ggctaagtct acgttgctgc gccatacacg ccatgagtta 360
gcaaaacttc ggctgctgct cgaggaggag tcccgtgagc agtaa 405

        <210> 175
        <211> 303
        <212> DNA

<210> E. Coli

<400> 175

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gtgagcagta aagtcgaacg tgaacgacgt aaggcgcaac tgcttagcca gatccagcaa      60
caacggttgg atctttccgc cagtcgtcgt gaatggctgg agacaacagg cgcttacgat     120
cgtcgctgga atatgctgct aagtctcgcg tcctggcgcg tggttggcag tagcgtgatg     180
gcgatctgga cgattcgcca tcctaatata ctgtctcgct gggccagacg cggttttggc     240
gtatggagcg cctggcgtct ggttaaaacg acccctcaag agcaacagct tcgcggttaa     300
```

<210> 176
<211> 483
<212> DNA
<213> E. Coli

<400> 176

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atgattctct ccatcgacag caagcagcgc aataccgcgc cattgcacaa aaaaacaatc      60
agcagcctga gttgcccagt ggagagtatg atgaaaaaat tagaagatgt tggtgtactg     120
gtagcgctga ttttaatgcc gattctcgtt attaccgctg gctggggaaa aattactggc     180
tacgcgggta ccaacaata tatggaagca atgggcgtcc cggttttat gctgccactg     240
gtgattctgc ttgagtttgg tgtgcggtctg gcaatcctgt tcggtttcct gactcgcacc     300
acagcccgt ttactgcggg cttcagcgtg ctgacggacg tttattttca cagcaactc     360
gctgaagcg tcaatcgct gatgttcatg aaaaacctga caattctgg cggattcctg     420
ctgctgtcaa ttacggtcc gggcgcgtat agcatcgacc gcctgctgaa taaaaagtgg     480
taa                                                                   483
```

<210> 177
<211> 591
<212> DNA
<213> E. Coli

<400> 177

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atgatccatga agacaaacgga aattgatgcc atctttgttaa atctcaataa ggctatcgat      60
gcccatcacc agtggctggt gagtatgttt cacagcgtgg cggcgagaga tgccagtaag     120
ccagaaataa cggataacca ttcttatgga ctgtgccagt ttgtcggtg gattgatcat     180
actggggcac tcgataacga tgaattacct tacgttggc taatggattc tgcccatcaa     240
catatgcata attytggcg ggaattaatg ctggctattg ttgaaatca ctgccaggac     300
ggcgcattcg acgccttcca ggagggggtg cttctttta ctgggcgatt aaccgattac     360
aaaatttatt tgttgacgat ccgtagcaat atggatgctt tgacgggtat gccgggtcgt     420
cgggtttctg atgaatcct tgatcatcag ttagcgaacg ctgagccctc gaatcttat     480
ttaatgttgt tcgatattga ccgattaaa ttggttaatg atacctaggg gcatttaatc     540
ggcgatgtaa cattacgcac cctggcaact cacttagcca gttggacgcg tgattacgaa     600
acggtttattc ggtacggggg cgaagaattc atcattattg tcaaagcggc taatgatgaa     660
gaagatgta gtgcaggcgt cagaatttgc cagttagtcg ataaccatgc catcacacat     720
tctgaagggc atatccacat tacggtgaca gcaggtgtga gtgggcaatt tcctgaagag     780
cctctgggtg tgttcattgg aagagcggac cgggcaatgt atgagggtaa gcaaaccgga     840
agaaatcgct gcatgtttat tgacgaacaa aatgtgatta accgagttta a                 591
```

<210> 178
<211> 612
<212> DNA
<213> E. Coli

<400> 178

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atgcgcttcc gtttgtgcc cggttttatt tcaccacctc cgggcttcgg tggtctcggc      60
tataccctta cacgagagc ttgtgtcaac atttcaatac cttacagtc ggagagttatt     120
gatatgttgg atgtatttac tccattgttg aaattttttg ctaacgacc actcgaaaga     180
cttatgtata cgattatcat ttttggtctc actctctggc tgatacgaa agagtttact     240
```

```
gtcgcattca atgcttatac tgaaatacct tggctctttc agattatcgt ttttgccttt       300
tctttcgtgg tcgccatttc cttctcaaga ttgcgagcac atattcaaaa gcattattca       360
ttactaccag agcaacgagt attgcttcgt ttatctgaga aagaaatcgc tgtatttaaa       420
gatttccttc aaacaggaaa tcttattatc acttctcctt gccgtaaccc ggttatgaaa       480
aaattagaac ggaaggggat cattcaacat cagagtgata gcgcaaactg ttcttattat       540
ctcgtcaccg aaaaatactc ccattttatg aagttattct ggaaaagcag gagtagacgt       600
tttaatcgtt ag                                                           612
```

<210> 173
<211> 177
<212> DNA
<213> E. Coli

<400> 173
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gtgcttttcc aaccatcggc cgcgcaccagt ttcggtttta aatgttttgc tcttggtata        60
cgtcatcgca gtgaagttc catcctggtc gggggaacacg cgcacacca gggattcgtt        120
gttgccgagg tcgattttttt gcattttgcg aatctcacat cttgttgcta cgtatag        177
```

<210> 180
<211> 4261
<212> DNA
<213> E. Coli

<400> 180
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atgagccgaa aaccagcggc gcgtcaggga gatatgactc agtatgggcg tcccattgtc        60
cagggtctgg catgtgtaag aattggcgcg cccacccggg ttggcgtctc ggtgtgtccg       120
ggcgggatga cttcgggcaa cccggtaaat ccgctgctgg gggcgaaggt gctgcccggc       180
gagacggacc ttgcgctgcc cggccgcgtg ccgttcattc tctcccgcac ctacagcagc       240
taccggacga agacgcctgc acggtggggc gtttttcggcc ccggctggaa agcgccttct       300
gatatcgct tacagctacg tgatgacgga ctgatactca acgacaaggg cgggcgggagc       360
attcacttg agcgcgtgtct gccggggtag gcggtgtaca gcgcagtga gtcaatgtgg       420
ctgtgtgcg gtgggtaagg aagcacagcc gacggccata cgctggcgcg gctgtggggg       480
ggcgtgcgg cggatatccg gttaagccg catctttacc tggcgacaa cagcgcacag       540
ggcgcgtggt ggatactgg gtggtctgac cgggtgccgg gttctgagga cgtactgcca       600
ggcgcgtgc cgcggtaccg ggtgcttacc gggatggcgg accgcttcgg cgggacgtg       660
agtacgggc gtgagccgc ccgtgacctg gccgggggaaa tcacggcgt gacggacggt       720
gcccggggggg agttccgtct ggtgctgacc acgcaggcgc agcgtgcgga agaggcccgc       780
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acactgcccg gtatcgaata cggcccgac agggtatcc gcctttcggc ggtgtggctg       900
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aggaaaccg gtgaactgct gggggtatat gacggcagca atagcgcaggt ggcggcttc      1020
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gacgggcagcg tcacgcgcag cgggtatgac cgggcaggaa ggctcacggg cgagaacgac      1320
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accacatcgg acgggcgga gacgaaattt tactataacg acggaaacca gctgacggcg      1440
gttgtgtccc cggacgggtct ggagagccgc cgggaatatg atgaacgggc caggctggta      1500
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aacgccacag gcgtacctgac ttccgttatc accccggacg gcaacggag cgagacacag      1860
tacgatcgt gggggaaagc ggtcagtacc acgcaggcg ggctgacgcg cagtatggag      1920
tacgatcctg ccggacgtgt catcagcctg accaacgaga acggcagcca cagcgtcttc      1980
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agttacgatg cgctggaccg gctggtacag caggcgggct ttgacgggcg gacgcaacgt    2040
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tggtactacg atgaatcgga ccgtatcact cacggcacgg tgaacggcga acgggcagag    2160
cagtggcagt atgatggcca cggctggctg acagacatca gccacctgag cgaaggccac    2220
cgtgttcccg tccactatgg ctatgacgat aaaggccgcc tgaccggcga atgccagacg    2280
gtggagaacc cggagacggg ggaactgctg tggcagcatg agacgaaaca cggatacaac    2340
gagcagggc tggcaaaccg cgtcacgccg gacagcctgc cgccggtgga gtggctgacg    2400
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cgggacaagc tgacccgtga gacgggttgcgg agcttcggca gcatggcagg cagtaatgcc    2520
gcatacgaac ttgaccagac atacacccc gcaggccagt tacagagcca gcaccctgaac    2580
agcctggtat atgaccgtga ctacgggttg agtgacaacg gcgacctggt gcgcatcagc    2640
ggcccgcac agacgcggga atacgggtac agcgccacgg gcaggctgga gagtgtgcgc    2700
acccctgaac cagacctgga catccgatc cggtatgcca cggacccgg gggcaacggg    2760
ctgccgtacc gggagctgca cccggacagt acactacag tgtggccgga taacggcatc    2820
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gacgcatcc cggcggggtgt gatacggacg gacgacgagc ggacccacca ctaccactac    2940
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cttaataata aaggagaata tattttatc agaaatagtg tcccgggatt gagttcacta    4260
tgcatatcgt atcatgatta a                                              4281
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atgaaatata gttcaatatt ttcgatgctt tcatttttta tactatttgc ctgtaatgag     60
acagctttt acggttctga tgaaaaatt attttatga ggtatgtgga aaaattacat    120
ttagatataat actctgttaa aaatacggta aaaactgaaa caatggcgat acaattagct    180
gaaatatatg ttaggtatcg ctatggcgaa cggattgcag aagaagaaaa accatattta    240
attacggact taccagatag ttgggttgtt gagggagcaa agttacctta tgaagttgcg    300
ggtggttat ttattatag aattaataag aaaaatggat gtgtttttgaa tttcctacat    360
agtaaatca                                                             369
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<213> E. Coli

<400> 182
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atgctggcgc tgatggatgc ggatggaaac attgcgtgga gcggggagta tgatgagtgg        60
ggcaaccagc tgaatgaaga gaacccgcat cacctgcacc agccgtaccg gctgccgggg       120
cagcagtatg ataaggagtc ggggctgtac tacaaccgga accggtacta cgatccgttg       180
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tatccgttga atcggtgaa tggtattgat ccattaggt taagtcccgc agatgtagcg         300
ctaataagaa gaaaagatca actaaaccaa caaagagcat gggatatatt atctgatact       360
tatgaagata tgaagagatt aaatttaggt gggactgatc aattttttcca ttgtatggca      420
tttttgtcag tgtctaaatt aaatgacgct ggtgtagcc gatcggcgaa agggctgggt        480
tatgaaaaag agattagaga ttacgggta aatctgttcg gtatgtacgg cagaaaagta        540
aagctatccc attctgaaat gattgaagat aataaaaaag actggctgt aaatgaccat        600
gggttggtat gtctatcaac aaacagattgc tcagatatat gtagtgatta tattaatcca      660
gagcataaaa aagatataa ggctttacaa gatgctggct atctcaagta a                711
```

<210> 183
<211> 281
<212> DNA
<213> E. Coli

<400> 183
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atgctggcta tctcaagtaa tctatcaaag atgataatat ttattttgc tattataatc        60
attgttttt tatgcgtaat tacttatctt tattatataca aagatgaatc tcttgtaagt       120
aaacatiaca taaactatat ggcaatacca gaaaatgatg gagtttttac atggctccca       180
gatttttttc cgaacgtagc ggtggatata tcaatataca caaatgtaga agatgattat       240
ttttttttta tcttttccta a                                                  261
```

<210> 184
<211> 182
<212> DNA
<213> E. Coli

<400> 184
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gtgagggcca gggaacaagt ggcgaaaatc gtatcaaaga atgatccaga tacaaaaaaa        60
ggtgggtgta aatatggtaa gataccaggg caaggggatg ggtaaaacc ttttttgtt        120
ggtgaaatta atcttacgca ttatcttata acaaatattg gagctggatt ggcctgatgct      180
tgtgcagagt aa                                                            192
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<210> 185
<211> 504
<212> DNA
<213> E. Coli

<400> 185
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atgccggtca acagcccgca ttatgggcgt tggcctcaac acgatttac gtcacttaaa        60
aaactcaggc cgcagtcggt aacctcgcgc atacagccgg gcagtgacgt catcgtctgc        120
gcggaaatgg acaacagtg gggctatgtc gggctaaat cgcgccagcg ctgcctgttt         180
tacgcgtatg acgtctctgg gaagacggtt gttgcgcacg tattcggtga acgcactatg        240
gcgacgcagg ggacctttat gagcctgctg tcacccttg acgtggtgat atggatgacg        300
gatggctggc cgttgtatga atccgcctg aagggaaagc tgcacgtaat cagcaagcga        360
tatacgcagc gaattgagcg gcataacctg aatctgaggc agcacctggc acggctggga      420
cggaagtcgc tgtcgttctc aaaatcggtg gagctgcatg acaaagtcat cgggcattat      480
ctgaacataa aaactatca ataa                                               504
```

<210> 186
<211> 278

<210> DNA
<213> E. Coli

<400> 126
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ggcaaaagca cctccggaca tcagcgctat ctctgctctc actgccgtaa aacatggcaa   120
ctgcagttca cttacacggc ttctcaaccc ggtacgcacc agaaaatcat tgatatggcc   180
atgaatggcg ttgatgccg ggcaacagcc cgcattatgg gcgttggcct caacacgatt   240
ttacgtcact taaaaacact aggccgcagt cggtaa   276

<210> 127
<211> 417
<212> DNA
<213> E. Coli

<400> 127
atgatgactt aaaccaaat aaataaatta ataaaaatga tgaatgattt agactatcca   60
tttgaagca cgttcaagga atcatttatt gaaagtataa tccaaataga atttaattct   120
aattcaacta attgcctgga gaagttatgt aatgaagtta gtattccttt taagaatcaa   180
cctgattact ttccttttttt aagagcaatg gatggattcg aagttaatgg attacgatta   240
tttagcctct cgattccaga acttccagtt aaaaaccttt ttgccgtaaa tgaattttat   300
agaaataatg atgattccat aaaccctgat ctacaagaac ggttagtgat cggggattat   360
agcatttcac tatttacctta tgacattaaa ggtgatgctg ccaacttact gatttag   417

<210> 128
<211> 1179
<212> DNA
<213> E. Coli

<400> 128
atgagtaata ttgtttaccc gacagtaacg ggagaacaac aaggaagcat ctccgcaggt   60
tgtgggactt ctagtctatc aggtaatcgt tggcagagcg ggcatgagga tgaaatatt   120
acattctcac tcttaaatat tattaataat acggggcttg gttcacagtt ccatggtata   180
acatttttgta aattaattga taaaagcact ccattatta ttaattccat taacaataat   240
gaacaattat tttggggatt tgacttctat cgaataaata gatttggtag attggaaaag   300
tattattata ataaaactaag aggcgctttt ttatcggcta ttcatcacca gatcattgaa   360
aaccaactgt atacagaaac aataactatt agttatgaat ttatctctg tcaacatctt   420
atgcaaaata cctagttcag ctatttggca ctccctgaaa attataacg tttgtttta   480
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ctgaccatcc ttgttgacgg taaagaaata aaagttaaag ctaggacgt acagcgtcac      240
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    <13> E. Coli

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<213> E. Coli

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<213> E. Coli

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<211> 93
<212> DNA
<213> E. Coli

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<210> 1 9
<211> 6 5
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<212> DNA
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<210> 2 1
<211> 5 9
<212> DNA
<213> E. Coli

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aatgccgctt gctcagttga tgcaggctct gctgatcaaa ccgttcagtt aggacaggtt   180
cgtaccgcat cgctggcaca ggaaggagca accagttctg ctgtcggttt taacatttag   240
ctgaattatt gcgatacgaa tgttgcatct aaagccgctg ttgccttttt aggtacggcg   300
attgatgcgg gtcaatacaa cgttctggct ctgcagagtt cagctgcggg tagcgcaaca   360
aacgttgttg tgcagatatca ggacagaacg ggtgctgcgc tgacgctgga tggtgcgaca   420
ttagttgcat aaaacaaccac ggaataacgga accaatacca ttccgttcca ggcgcgttat   480
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<210> 212
<211> 648
<212> DNA
<213> E. Coli

<400> 102

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agattatttc tattacgcgtc gttgctgcca atgtttgctc tggccggaaa taaatggaat   180
accacgttgc cttgcggaaa tatgcaattc caggcggtca ttattgcgga aacttgcggg   240
attgaagtcg gttataaaaca aatgacggtc aatatgggg aaatagcag taacggttt   300
catgcggttg gtgaagatag cgcacggtg ccttttgtta ttcatttacg ggaatgtagc   360
acggtggtga gttaaagtgt aggtgtggcg cttcaaggtg tcgcggatgg taaaaatccg   420
gatgtgcttt ctttgggaga gggggccaggg atagccacca atattggcgt agcgttgttt   480
gatgatataag gaaacctcgt accgattaat cgtcctccag caaactggaa acggcttat   540
tcaggcctta cttcgctaca tttcatgcc aaatatcgtg ctacgggcg tcgggttact   600
ggcggcctcg ctaatgccca ggcctggttc tctttaacct atcagtaa             648
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<210> 103
<211> 726
<212> DNA
<213> E. Coli

<400> 103

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ggttcgactc gcgtaattta tcggcaggg caaaaacaag agcaacttgc cgttacaaa   180
aatgatgtag ataagtaccta tttaattcaa tcatgggtgg aaaatgccga tggtcgtaag   240
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ttacgtattc ttgatgcaac aaaataacaa ttgccacagg accggaaaag tttattcgg   360
atgaacgtta aagtgattcc gtcaatggat aaatcaaaat tgactgagaa tacgctacag   420
ctgcaattca tcagcgcgat taaactgtac tatcgcccgg ctaaattagc gttgccaccc   480
gatcagguccg cagtaaaatt aagatttcgt cgtagcgcga attctctgac gctgattaac   540
ccgacacct attacttgac ggtaacagag ttgaatgccg gaaccggt tcttgaaaat   600
gcattgtggc ctccaatggg cgaaagcacg gttaaattgc cttctgatgc aggaagcaat   660
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gaataa                                                             726
```

<210> 104
<211> 657
<212> DNA
<213> E. Coli

<400> 104

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atgtcatatc tgaatttaag actttaccag cgaaacacac aatgcttgca tattcgtaag    60
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-74-

catcgtttgg ctggtttttt tgtccgactc gttgtcgcct gtgcttttgc cgcacaggca   120
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gtggccgatt tatccgcgtt tgaaaatggg caagaattac cgccagggac gtatccgctc   240
gatatctatt tgaataatgg ttatatggca acgcgtgatg tcacatttaa tacgggcgac   300
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acggcttctg tcgccggtat gaatctgctg ccggatgatg cctgtgtgcc attaaccaca   420
atggtccagg acgctactgc gcatctggat gctggtcagc agcgactgaa cctgacgatc   460
cctcaggcat ttatgagtaa tccgcgcgt ggttatattc ctcctgagtt atgggatccc   540
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gggggtaaca gccattatgc atatttaaac ctacagagtg ggttaaatat tggtgcgtgg   660
cgtttacgcg acaataccac ctggagttat aagagtagcg acagatcatc aggtagcaaa   720
aataaatggc agcatatcaa tacctggctt gagcgagaca taataccgtt acgttcccgg   780
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tataatagta cggtgcacc ggggccttt accatcaacg atatctatgc cgccaggtaat   1020
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ctcgttata acaaacgcgg gaaattacaa ctcaccgtta ctcagcaact cgggcgcaca   1620
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caattccagg ctggattaaa tactgcgttc gaagatatca actggacgct cagctatagc   1740
ctgacgaaaa agcctggca aaaaggacgg gatcagatgt tagcgcttaa cgtcaatatt   1800
cctttcagcc actggtgcg ttctgacagt aaatctcagt gggacatgc cagtgccagc   1860
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ctgccaccag agagtcagca gcagttatta acccagctat cagctgaatg tcgttaa   2637

atgagaaaca aacctttta tcttctgtgc gctttttgt ggctggcggt gagtcacgct   60
tggctgcgg atagcacgat tactatccgc ggtatgtca gggataacgg ctgtagtgtg   120
gccgctgaat caaccaatt tactgtgat ctgatggaaa acgcggcgaa gaaatttaac   180
aacattggcg cgacgactcc tgttgtctca cttcgtattt tgctgtcacc ctgtggtaat   240
gccgttcctg ccgtaaaggt tgggttact ggcgctgcag atagccacaa tgccgaacctg   300
cttgcacttg aaaatacggt gtcagcggct tcggggactgg gaatacagct tctgaatgag   360
cagcaaaatc aaaatacccct taatgctca tcgtccgcgc tttcgtggac gaccctgacg   420

ccgggtaaac caaatacggt gaattttttac gcccggctaa tggcgacaca ggtgcctgtc   480
actggggggc atatcaatgc cacggctacc ttcactcttg aatatcagta a   531

<210> 206
<211> 504
<212> DNA
<213> E. Coli

<400> 206
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gttccaccca ccaatgccac ggttgatctc ggcgatttca atctttttag ccttatgtct   180
gccgggtcag catcggccgc gcatgatgtt gcgcttgagt cgactaattg tccggtggga   240
acgtcgaggg tcactgccag cttcagcggg gcagccgaca gtaccggata ttataaaaac   300
cagggacca cgcaaaaaca ccagttagag ctacaggatg acagtggcaa cacattaatt   360
actggccaa ctaaaacagt tcaggtggt gattcctcac aatcagcgca cttccgtta   420
caggtcagag cattgacagt aaatggcgga gccactcagg gaacccattca ggcagtgatt   480
agcatcacct atactacag ctga   504

<210> 207
<211> 903
<212> DNA
<213> E. Coli

<400> 207
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tcattcgcct gtaaaacggc caatggtacc gctatccta ttggcggtgg cagcgcaat   120
gtttatgtaa atcttcgcg cgtcgtgaat gtggggcaaa aactggtcgt ggatctttcg   180
aagcaaatct tggccataa cgattatccg gaaaccatta cagactatgt cacactgcaa   240
cgaggctgg cttatggcgg cgtgttatct aattttttcg ggaccgtaaa atatagtggc   300
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gataagcgt gccggttggc gctttattg acgcctgtga gcagtgcggg cggggtgggg   420
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gatgatttct agttcgtgtg taatatttac gccaataatg atgtggtggt gcctactggc   540
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ccaattcctt ttaccgttta ttgtgcgaaa agccaaaac ttggggtatta cctctccggc   660
acaaccctag attgggcaa ctcgattttc accaatacg cgtcgtttc acctgacag   720
gggtgaggcg ttcagttgac gcgcaacggt accgattattc cagcggaataa cacggtatcg   780
ttaggactac taggggactttc gggggtgagt ctgggattaa cggcaaatta ttgcacgtac   840
gaggggtacgg tcactgcagg gaatgtgcaa tcgattattg gcgtgacttt tgtttatcaa   900
taa   903

<210> 208
<211> 1461
<212> DNA
<213> E. Coli

<400> 208
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tgggcggta atcctggttt ctggccattg cagttactcg ataaagtaac tccgtcacag   180
tgggctgaa tcgtgcgct gggagcctg gttttggcc tgctgacgta tctgacaaat   240
cctttatttca agttaaaga agacaggcgt aaggctgcga gaggagagta atccaatgac   300
tcaagatat gacctggttg tgaaaggagt ccgtaatttt gagaataaag ttacggtaac   360
tgtacgctta cagacaaag aacgctttga cggtgaaatt tttgacctgg atgtcgccat   420
ggacggtgtt gaaggagctg cgctggagtt ttatgagca gcagccagaa ggagcgccg   480
gcaagttttc ctggaagtag cagaaaaatt gtcagaaaaa gttcagtctt atctgcagca   540

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tcagtattcc tttaagattg aaaatcctgc caataagcac gagcgtcctc atcataaata      605
tctatgaaca caaaaactaa ataoggctg tcggctgccg ttctggcgct gattggtgct      660
ggcgatctg ctcctcagat acttgaccag tttctggacg aaaaagaagg taaccacaca       7.0
atggcacc gcgatggttc tggcatatgg accatctgtc ggggtgcac agtggtggat         7.0
ggaaaaaacc ttttttccaa tatgaaactg tcgaaggaaa aatgcgacca ggtcaacgcc       840
attgagcgt ataaggcgct ggcatgggtg gagcgcaata ttaaagtacc actgaccgaa        900
ccacaaaag ggggtatcgg gtcattttgt ccctataaca ttggcccgg taagtgtttc         960
ccgtctgact tttataagcg gctgaatgct ggtgatctgta aagtgcatg cgaagcgatt       1000
cgctggtga ttaaggatgg cggacgcgat tgcgcattc gttcaaataa ctgttacggt        1080
caggttattc gtcgtgacca ggagagcgca ttaacctgct gggggatага acagtgaatc      1140
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ttaaagtgtc gcaacagaaa tctgctgaaa tttctgccag ggctgcttat ctgtctgata      1380
gtgttaacca gttgctgtcg gaagcaaaaa aatatgccac acgccttgac gcagcgaagc       1440
atacgcttaa tcttgctcgt gccgtcagag gcaaaacaac caaaaccgcc gaaggaatgc       1500
tgaccaccat gtcggagtat attgcagcag aagctcagct ttatgctgaa aatgctgacg       1560
aagcgtacat ctcaggagtc acttgtcaac agatctatga atctttaaga gataaaaagc       1620
atcaaatgta g                                                            1631
```

```
atgaacacaa aaatcagata cgggctgtcg gctgccgttc tggcgctgat tggtgctggc      60
gcatctgtctc ctcagatact tgaccagttt ctggacgaaa aagaaggtaa ccacacaatg      120
ggcataccg atggttctgg catatggacc atctgtcggg gtgccacagt ggtggatgga       180
aaaaccttt ttccaatat gaaactgtcg aaggaaaaat gcgaccaggt caacgccacc        240
gagcgtaata aggcgctggc atgggtggag cgcaatatta aagtaccact gaccgaacca       300
caaaaaggg gtatcgggtc attttgtccc tataacattg gcccggtaa gtgtttcccg        360
tctgacgttt ataagcggct gaatgctggt gatctgtaaag gtgcatgcga aggattggc      420
tggtggatta aggatggcgg acgcgattgc gcattcgtt ccaaataactg ttacggtcag       480
gttattcgtc gtgaccagga gagcgcatta acctgctggg ggatagaaca gtga            534
```

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atgactcaag attatgaaact ggttgtgaaa ggagtccgta atttgagaa taaagttacg      60
gtaactgtag cttacagga caaagaacgc tttgacggtg aaattttga ctggatgtc        120
gccatggccg gtgttgaagg agctgcgctg gagttttatg aggcagagc cagaaggagc       180
gtcggcaag tttcctgga agtagcagaa aaattgtcag aaaaagttga gtcttatctg       240
cagcatcgt attcctttaa gattgaaaat cctgccaata agcagagcg tcctcatcat        300
aaatatctat ga                                                          312
```

```
gtgctgtcaa aactacccg tagactccga tcttttcaaa catattgcac catcgtgta         60
catcggggtc aggatatgaa atcaatggat aagttaacaa caggtgttgc ctatggcaca       120
```

```
tcggcgggta atgctggttt ctgggcattg cagttactcg ataaagtaac tcgctcacag      180
tgggctgcaa tcgctgtgct gggtagcctg gtttttggcc tgctgacgta tctgacaaat      240
ctttattttca agattaaaga agacaggcgt aaggctgcga gaggagagta a              291


     <210> 212
     <211> 216
     <212> DNA
     <213> E. Coli

     <400> 212
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attcctcctg ttgatggtag taaagatgtg tttgttcatt ttttctgcat tcagaatgat      120
aattatcgaa cctatttga  aggtcaaaag gttacccttt ctatagagag tggtgctaaa      180
ggtcctgcag ctgcaaatgt catcattact gattaa                                216


     <210> 213
     <211> 1017
     <212> DNA
     <213> E. Coli

     <400> 213
atgtttgtca tcttgagcca tagaacaggg ttcatcatga gtcatcaact tacccttgcc       60
gacagtgaat tcatcagtaa gcgccgtcag acgagaaaag agattttctt gtcccgcatg      120
gagcagattt tcttcatggca aaacatggtg gaagtcatcg agccgtttta ccccaaggct      180
ggtaatggcc ggcgacctta tccgctggaa accatgctac gcattcactg catgcagcat      240
tggtacaaca ttacccgatgg cggcgatgaa gatgctctgt acgaaatcgc ctccatgcgt      300
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cgccaactgt tgtacgacga tcaactggcc cgccaattgt tcaagaccat caatcgctgg      420
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tgaccaact  cgtccaagaa caaagatcag caacgcgatc cggagatgca tcagaccaag      540
aaaggctatc acgggcactc tggcatgaag gcccacattg gtgtcgatgc caagagtcgg      600
ctgaccaca gcgtggtcac cacccgcgcc aaggagcatg acctcaatca gctgggtaat      660
ctgctgtatg gagaggagca atttgtctca gccgatgccg gataccaagg ggcgccacag      720
cggggatagg tctccgaggt ggatgtggac tggctgatcg ccgagcgccc cggcaaggta      780
agaacctga  aacagcgatcc acgaagaac aaaacggcca tcaacatcga atacatgaaa      840
gccagcatcc ggggccaggg ggagccaccca tttcgcatca tcaagcgaca gttcggcttc      900
gtgaaatcca ggcacaaggg gttgctgaaa aacgataacc aactggcgat gttattcacg      960
ctggccaacc tgtttcgggc ggaccaaatg ataagtcagt gggagagatc tcactaa         1017


     <210> 214
     <211> 473
     <212> DNA
     <213> E. Coli

     <400> 214
atggtatata tataatactg tccccaagga catgaagact acatcaaaaa attactcgaa       60
aatcttaatg ctgacgatga gcaatacaag attatcgtac gcgacaacaa agatctctc      120
ttattgaaac aaatatgcca gcattatca  ggcctggaca atattagtgg aggtgtatac      180
ggctttttgtc attataataa tattgcggtg gcgtatgtaa aggaaaaata tagacccgca      240
gatgatgatt acatttttgtc ttgaatccc  gatatcatca tgaagcatga tgatttgctg      300
acatatatta aaatgtgtga aagtaagctg tatgctttta gtacattatg cctgttccga      360
gatgaagcga aatcttaca  tgattatttcc gtaagaaaat ttcctgtgct ttctgatttt      420
attgtgttat ttagttagg  gattaaggaa ggtgcgaaca agtccctgat atga            474


     <210> 215
     <211> 1119
     <212> DNA
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<212> E. Coli

<400> 215

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atgggaaaaa gcatagtgt tgtttctgcg gtcaatttta ccactgggg tccatttacc      60
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gtccattctc ctaaagagtt aaaagaaagt tatccatggg ttaaattcat tgagtttcct     180
gaggttaaaa ggtcgtggct aaaagtttg cactttgaat atgtagtttg taaaaaactt     240
tcaaaagagc tgaatgctac gcattggatt tgtctgcatc atattacggc caatgtcgtc     300
agtaaaaaaa gatatgtgta ttgtcatcaa cctgcacctt ttcataaaaa aatttttattc     360
cgtgaaattc ttatggagcc tagtttttc ttatttaaaa tgctataggg gctgatatat     420
aaaataaaca ttaaaaaaaa tactgcagtg tttgttcaac aattctggat gaaagaaaaa     480
tctatcaaaga aataccatc aaaataacac attgtcagtc ggccagaaat caaattattc     540
gataaaaagc aagcttactga tgatgattct caatttaaga ataaccctc tgagttgaca     600
atattttacc ctgctgttcc acgagtatta aaaaaattga agcttattat tagtgcagca     660
aggaaattga aagaacctac caatattaaa tttctgctca ctatcagtgg tacagaaaaa     720
gcgtatgcaa aatatattat cagtcttgca gaaggactgg ataatgtcta tttcctgggg     780
tagttggata aagaaaaaaa cgatcattgt tataatattt cagatatagt ttgtttccc     840
tctaggttag aaacatgggg attgccgttg tctgaagcta aagagcgagg taagtgggta     900
ttagcatcag attccccatt tactagagaa actcttggta gttatgaaaa gaaagctttt     960
tctgattcta ataacgatga catgttagtt aaacttatta ttgacttcaa aaaaggtaac    1020
ctgaaaaaag atatctctga tgcaaatttc attatatgta atgaaaatgt attagttggg    1080
tttgatcaaa tagttaattt tattactgaa gaacattga                           1119
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<211> 216
<211> 591
<212> DNA
<213> E. Coli

<400> 216

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cgcaatgatc gtagcattaa ttttggtgaa aattcacaa gtgggagtcgg tcccaggctg     180
gatgcatttc gagctgtcgt gattttttt tccgataatg tgcaagtcaa cgactatgtt     240
catatcgcct caattgagag cgttacgata ggtcgggata cgcttattgc aagtaaagta     300
tttattaccg atcataatca cggttccttt aagcactctg atccaatgag ttcgccaaat     360
atacctgaac acatgcgcac gttggaatct tcagctgttg taattggcca gaggggttgg     420
ttgggtagga atgtgacgtt tttgctgga acaattattg gcaatggagt cgtagtcggc     480
gccaattctg ttgttagagg ttctattccc gaaaatactg tcattgcggg agtaccagca     540
aaaatcatca agaaatacaa tcatgagacc aaattatggg aaaaagcata g             591
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<211> 217
<211> 993
<212> DNA
<213> E. Coli

<400> 217

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<213> E. Coli

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<213> E. Coli

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<210> 226
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<212> DNA
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<210> 227

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aatggcaaac tgttgatgc ttgcgatctg attgaaaacg acgacaact gtcgatcatt       180
acgccaaag a tgaagaagg tctggagatc attcgtcact cctgtgcag cctgttaggg       240
caacgcgatta aacaactttg gcggcatacc aaaaatggcaa tcggcccggt tattgacaac       300
ggttttatt a tgacgttga tcttgaccgc acgttaaccc aggaagtgtt cgaagcctcc       360
gagaagctga t tgcatgagcc tgctgagaaa aactacgacg tcattaagaa gaaagtcagc       420
tggcacaag c tcgtgaaa tttgccaac cgtggggaga gctacaaagt ctccattctt       480
gacgaaaaca t tgcccatga tgacaagcca ggtctgtact tccatgaaga atatgtcgat       540
atgtgcacg g tcgcgcagc acggaacatg cgtttctgcc atcattcaa actaatgaaa       600
acggacatgg c ttactggcg tggcgacagc aacaacaaaa tgttgcaacg tatttacggt       660
acggcgtggg c agacaaaaa agcacttaac gcttacctgc aggggctgga agaagccgcg       720
aaacgcgacc a tcgtaaat cggtaaacag ctcgaccttgt accatatgca ggaagaagcg       780
cccggtatgg t attctggca caacgacggc tggacatcat tccgtgaact ggaagtgttt       840
gttcgttcta a ctgaaaga gtaccagtat caggaagtta aaggtccgtt ccatgatggac       900
cgtgcctgt g ggaaaaaac cggtcactgg gacaactaca aagatgcaat gttcaccaca       960
tcttctgaga a cgtgaatta ctgcattaag ccgatgaact gcccgggtca cgtacaaatt      1020
ttcaacaggg t tctgaagtc ttatgcgat ctgccgctgc gtatggccga gtttggtagc      1080
tggcacgta a tgagccgtc aggttcgtc catggcctga tgcgctgcg tggatttacc      1140
caggatgacg c tgcatatctt cctgtactgaa gaacaaaatc gggatgaagt taacggatgt      1200
atccgtttag t tatgatat gtacagcact tttggcttcg agaagatcgt cgtcaaatc      1260
tccactcgtc c tgaaaaacg tattggcagc gacgaaatgt gggatcgtgc ttaggcggac      1320
ctgggcatg c gcgtgaaga aaacaacatc ccgtttaat attaactggg tgaaggcgtc      1380
ttctaccgtc c cgaaaattga atttaccctg tatgactgcc tcgatcgtgc atggcagtgc      1440
ggtacaatac a gtggtcac ctctttgccg tctcgtctga gcgcttctta ttgtaggcgaa      1500
gacaatcaac g taaagtacc ggtaatgatt caccgcgcaa ttctgggtc gatggaagt      1560
ttcatcgta t tctgaccga agagttccgt ggttttcttc cgacctggct tggcccggt      1620
caggttgtta t ctgaatat tacccgatca cagtctgaat acgttaacga attgacgaa      1680
aaactatcaa a tacgggtat tcgtgttaaa gcagacttga aaatgagaa gattggcttt      1740
aaaatcgccg a gcacactttt gcgtcgcgtc ccatatatgc tggtctgtgg tgataaagag      1800
gtggaacag g caaagttgc cgttcgcacc cgccgtggta aagacctggg aagcatggac      1860
gtaaatcaac t ttatcgagaa gctgcaacaa gagattcgca ccgccagtct taaacaattg      1920
gaggaataa                                                              1929
```

<210> 138
<211> 1953
<212> DNA
<213> E. Coli

<400> 138
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atgactaaac a taatgatta catgccatc ggcggcggca gcggcggtat cgcctccatc        60
aaccgcgtgg g ttatgtacgg ccagaaatgt gcgctgattg aagcaaaga gctggggcggc       120
accggctaa a tctttggctg tgtgcgaaaa aagtgatgt ggaagcggc ggaaatccgt       180
gaagcgatcc a ttgtacgg cccggattat ggttttgata ccactataaa taaattcaac       240
tgggaaagt t tatcgccag ccgtaccgcc tatatcgacc gtattcatac ttcctatgaa       300
aacgtttcg g taaaatat cgttgatgta atgaaaggc ttgccgctt cgttgatgcc       360
aaaaatcgg a ttgtaaacgg cgaaaccatc acggcgatc atatctgat cggcacaggc       420
ggtcgtctga g acaccggga tattcggggc gtggaatacg gtattgatcc tgatggcttc       480
ttgccctc c tgtgtttgcc agagcgcgtg ggggttgttg cgcggggtta catgccggtt       540
gagctggggg g tgtgattaa cggcctcggc ggaaaacgc atctgtttgt gggtaaacat       600
ggcgcgtgc g tagcttcga ccgatgatt tcgaaaagc tggtcaagt gatgaaagcc       660
gaaggcccgc a tcgtacgca caacgccatc ccgaaagcgg tagtgaaaaa taccgatggt       720
```

agcctgacgc tggagctgga agatggtcgc agtgaaacgg tggattgcct gatttgggcg   780
attggtcgcg agcctgccaa tgacaacatc aacctggaag ccgctggcgt taaaaactaac   840
gaaaaaggct atatcgtcgt cgataaatat caaaacacca atattgaagg tattttacgcg   900
gtgggcgata acaggggttgc agtggagctg acaacggtgg cagttgcagc gggtcgccgt   960
cctctctaaac ggctgtttaa taaacaagccg gatgagcatc tggattacag caacattccg   1020
aggctggtct tcagccatcc gccggattggt actgttggtt taacggaacc gcaggcgcgc   1080
gagcagtatg gcgacgatca ggtgaaagtg tataaatcct cttttcacgcg gatgtatacc   1140
gccgtcacca cttaacgcca gccgtcgcgc atgaagctgg tgtgcgttgg atcggaagag   1200
aagatttccg gtattcacgg cattggcttt ggtatggacg aaatgttgca gggcttcgcg   1260
gtgccgttga agatgggccgc aaacaaaaaa gacttcgaca atacgcgcgc cattcacccca   1320
acggcggcag aagagttcgt gacaatgcgt taa   1353

gtaccgagtc acacgcctaa gcgtgctccc actgctttgta cgtacacggt ttcaggttct   2400
tttcactcc cctcgccggg gttcttttcg cctttcctc acggtactgg ttcactatcg   2460
gtcagtcagg agtattagc cttggaggat ggtcccccaa tattcagaca ggataccag   2520
tgtccggcc tactcatcga gctcacagca tgtgcatttt tgtgtacggg gctgtcaccc   2580
tgtatcgcg gccttccag acgttccac taacacacac actgattcag gctctgggct   2640
gctcccgtt cgctcgcgg tactggggga atctcggttg atttctttc ctcggggtac   2700
ttagatgttt cagttcccc ggttcgcctc attaacctat ggattcagtt aatgatagtg   2760
tgtcgaaaca caacgggttt ccccattcgg aaatcgccgg ttataacggt tcatatcacc   2820
ttaaccgagg ttatcgcaga ttagcacgtc cttcatcgcc tctgactgcc agggcatcca   2880
ccgtgtacgc ttagtcgctt aacc   2904

        <210> 140
        <211> 120
        <212> DNA
        <213> E. Coli

        <400> 140
atgcctggca gttcctact ctcgcatggg gagacccca actaccatcg gcgctacggc   60
gtttcacttc tcgcttcggc atggggtcag gtgggaccac cgcgctagg ccgccaggca   120

        <210> 141
        <211> 76
        <212> DNA
        <213> E. Coli

        <400> 141
gtccccttcg tctagagggc caggacacct cccttcacg gcggtaacag gggctcgaat   60
cccctagtgg atgcca   76

        <210> 142
        <211> 1549
        <212> DNA
        <213> E. Coli

        <400> 142
aaattgaaga gtttgatcat ggctcagatt gaacgctggc ggcaggccta acacatgcaa   60
gtcgaacggt aacaggaagc agcttgctgc ttcgctgacg agtggcggac gggtgagtaa   120
tgtctgggaa gctcctgat ggagggggat aactactgga aacggtagct aataccgcat   180
aatgtcgcaa gaccaaagag ggggaccttc gggcctcttg ccatcggatg tgcccagatg   240
ggattagctt gttggtgggg taaggctca ccaaggcgac gatccctagc tggtctgaga   300
ggatgaccag ccacactgga actgagacac ggtccagact cctacgggag gcagcagtgg   360
ggaatattgc acaatgggcg caagcctgat gcagccatgc cgcgtgtatg aagaaggcct   420
tcgggttgta aagtactttc agcggggagg aagggagtaa agttaatacc tttgctcatt   480
gacgttaccc gcagaagaag caccggctaa ctccgtgcca gcagccgcgg taataccgag   540
gtgcaagcg ttaatcggaa ttactgggcg taaagcgcac gcaggcggt tggttaagtc   600
agatgtgaaa tccccgggct caacctggga actgcatctg atactggcaa gcttgagtct   660
cgtagagggg ggtagaattc caggtgtagc ggtgaaatgc gtagagatct ggaggaatac   720
cggtggcgaa ggcggccccc tggacgaaga ctgacgctca ggtgcgaaag cgtggggagc   780
aaacaggatt agataccctg gtagtccacg ccgtaaacga tgtcgacttg gaggttgtgc   840
ccttgaggcg tggcttccgg agctaacgcg ttaagtcgac cgcctgggga gtacggccgc   900
aaggttaaaa ctcaaatgaa ttgacggggg cccgcacaag cggtggagca tgtggtttaa   960
ttcgatgcaa cgcgaagaac cttacctggt cttgacatcc acggaagttt tcagagatga   1020
gaatgtgcct tcgggaaccg tgagacaggt gctgcatggc tgtcgtcagc tcgtgttgtg   1080
aaatgttggg ttaagtcccg caacgagcgc aacccttatc cttgttgcc agcggtccgg   1140
ccgggaactc aaaggagact gccagtgata aactggagga aggtggggat gacgtcaagt   1200
catcatggc ccttacgacc agggctacac acgtgctaca atggcgcatac aaagagaagc   1260
gacctcgcga gagcaagcgg acctcataaa gtgcgtcgta gtccggattg gagtctgcaa   1320

```
ctgactcca tgaagtcgga atggctagta atcgtggatc agaatgccac ggtgaatacg   1380
ttccgggcc ttgtacacac cgcccgtcac accatgggag tggttgcaa aagaagtagg   1440
tagcttaacc ttcgggaggg cgcttaccac tttgtgattc atgactgggg tgaagtcgta   1500
acaaggtaac cctaggggaa cctgcggttg gatcacctcc ttaccttaa             1549
```

<210> 243
    <211> 221
    <212> PRT
    <213> E. Coli

    <400> 243
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Met Asn Val Phe Ser Gln Thr Gln Arg Tyr Lys Ala Leu Phe Trp Leu
1               5                   10                  15
Ser Leu Phe His Leu Leu Val Ile Thr Ser Ser Asn Tyr Leu Val Gln
                20                  25                  30
Leu Pro Val Ser Ile Leu Gly Phe His Thr Thr Trp Gly Ala Phe Ser
            35                  40                  45
Phe Pro Phe Ile Phe Leu Ala Thr Asp Leu Thr Val Arg Ile Phe Gly
        50                  55                  60
Ala Pro Leu Ala Arg Arg Ile Ile Phe Ala Val Met Ile Pro Ala Leu
65                  70                  75                  80
Leu Ile Ser Tyr Val Ile Ser Ser Leu Phe Tyr Met Gly Ser Trp Gln
                85                  90                  95
Gly Phe Gly Ala Leu Ala His Phe Asn Leu Phe Val Ala Arg Ile Ala
                100                 105                 110
Thr Ala Ser Phe Met Ala Tyr Ala Leu Gly Gln Ile Leu Asp Val His
            115                 120                 125
Val Phe Asn Arg Leu Arg Gln Ser Arg Arg Trp Trp Leu Ala Pro Thr
        130                 135                 140
Ala Ser Thr Leu Phe Gly Asn Val Ser Asp Thr Leu Ala Phe Phe Phe
145                 150                 155                 160
Ile Ala Phe Trp Arg Ser Pro Asp Ala Phe Met Ala Glu His Trp Met
                165                 170                 175
Glu Ile Ala Leu Val Asp Tyr Cys Phe Lys Val Leu Ile Ser Ile Val
                180                 185                 190
Phe Phe Leu Pro Met Tyr Gly Val Leu Leu Asn Met Leu Leu Lys Arg
            195                 200                 205
Leu Ala Asp Lys Ser Glu Ile Asn Ala Leu Gln Ala Ser
        210                 215                 220
```

    <210> 244
    <211> 119
    <212> PRT
    <213> E. Coli

    <400> 244
```
Met Ile Arg Trp Met Asn Glu Pro Leu Trp Pro Phe Ile Glu Arg Lys
1               5                   10                  15
Lys Ser Met Arg Asn Leu Val Lys Tyr Val Gly Ile Gly Leu Leu Val
                20                  25                  30
Met Gly Leu Ala Ala Cys Asp Asp Lys Asp Thr Asn Ala Thr Ala Gln
            35                  40                  45
Gly Ser Val Ala Glu Ser Asn Ala Thr Gly Asn Pro Val Asn Leu Leu
        50                  55                  60
Asp Gly Lys Leu Ser Phe Ser Leu Pro Ala Asp Met Thr Asp Gln Ser
```

65   70   75   80

```
      65                  70                  75                  80
Gly Lys Leu Gly Thr Gln Ala Asn Asn Met His Val Trp Ser Asp Ala
                    85                  90                  95
Thr Gly Gln Lys Ala Val Ile Val Ile Met Gly Asp Asp Pro Lys Glu
                   100                 105                 110
Asp Leu Ala Val Leu Ala Lys Arg Leu Glu Asp Gln Gln Arg Ser Arg
                   115                 120                 125
Asp Pro Gln Leu Gln Val Val Thr Asn Lys Ala Ile Glu Leu Lys Gly
     130                 135                 140
His Lys Met Gln Gln Leu Asp Ser Ile Ile Ser Ala Lys Gly Gln Thr
     145                 150                 155                 160
Ala Tyr Ser Ser Val Ile Leu Gly Asn Val Gly Asn Gln Leu Leu Thr
                   165                 170                 175
Met Gln Ile Thr Leu Pro Ala Asp Asp Gln Gln Lys Ala Gln Thr Thr
                   180                 185                 190
Ala Glu Asn Ile Ile Asn Thr Leu Val Ile Gln
     195                 200
```

```
<211> 245
<211> 244
<212> PRT
<213> E. Coli

<400> 244
```

```
Met Ala Asn Met Phe Ala Leu Ile Leu Val Ile Ala Thr Leu Val Thr
 1                   5                  10                  15
Gly Ile Leu Trp Cys Val Asp Lys Phe Phe Phe Ala Pro Lys Arg Arg
                    20                  25                  30
Glu Arg Gln Ala Ala Ala Gln Ala Ala Ala Gly Asp Ser Leu Asp Lys
                    35                  40                  45
Ala Thr Leu Lys Lys Val Ala Pro Lys Pro Gly Trp Leu Glu Thr Gly
     50                  55                  60
Ala Ser Val Phe Pro Val Leu Ala Ile Val Leu Ile Val Arg Ser Phe
 65                  70                  75                  80
Ile Tyr Glu Pro Phe Gln Ile Pro Ser Gly Ser Met Met Pro Thr Leu
                    85                  90                  95
Leu Ile Gly Asp Phe Ile Leu Val Glu Lys Phe Ala Tyr Gly Ile Lys
                   100                 105                 110
Asp Pro Ile Tyr Gln Lys Thr Leu Ile Glu Thr Gly His Pro Lys Arg
                   115                 120                 125
Gly Asp Ile Val Val Phe Lys Tyr Pro Glu Asp Pro Lys Leu Asp Tyr
                   130                 135                 140
Ile Lys Arg Ala Val Gly Leu Pro Gly Asp Lys Val Thr Tyr Asp Pro
     145                 150                 155                 160
Val Ser Lys Glu Leu Thr Ile Gln Pro Gly Cys Ser Ser Gly Gln Ala
                   165                 170                 175
Cys Glu Asn Ala Leu Pro Val Thr Tyr Ser Asn Val Glu Pro Ser Asp
                   180                 185                 190
Phe Val Gln Thr Phe Ser Arg Arg Asn Gly Gly Glu Ala Thr Ser Gly
                   195                 200                 205
Phe Phe Glu Val Pro Lys Asn Glu Thr Lys Glu Asn Gly Ile Arg Leu
     210                 215                 220
Ser Glu Arg Lys Glu Thr Leu Gly Asp Val Thr His Arg Ile Leu Thr
     225                 230                 235                 240
Val Pro Ile Ala Gln Asp Gln Val Gly Met Tyr Tyr Gln Gln Pro Gly
                   245                 250                 255
```

Gln Gln Leu Ala Thr Trp Ile Val Pro Pro Gly Gln Tyr Phe Met Met
        260   265   270
Gly Asp Asn Arg Asp Asn Ser Ala Asp Ser Arg Tyr Trp Gly Phe Val
        275   280   285
Pro Glu Ala Asn Leu Val Gly Arg Ala Thr Ala Ile Trp Met Ser Phe
        290   295   300
Asp Lys Gln Glu Gly Glu Trp Pro Thr Gly Leu Arg Leu Ser Arg Ile
305   310   315   320
Gly Gly Ile His

    - 210 - 246
    - 211 - 544
    - 212 - PRT
    - 213 - E. Coli

    - 400 - 246
Met Thr Ile Thr Lys Leu Ala Trp Arg Asp Leu Val Pro Asp Thr Asp
1   5   10   15
Ser Tyr Gln Glu Ile Phe Ala Gln Pro His Leu Ile Asp Glu Asn Asp
                    20   25   30
Pro Leu Phe Ser Asp Thr Gln Pro Arg Leu Gln Phe Ala Leu Glu Gln
            35   40   45
Leu Leu His Thr Arg Ala Ser Asn Ser Phe Met Leu Ala Lys Ala Pro
    50   55   60
Glu Glu Ser Glu Tyr Leu Asn Leu Ile Ala Asn Ala Ala Arg Thr Leu
65   70   75   80
Gln Ser Asp Ala Gly Gln Leu Val Gly Gly His Tyr Glu Val Ser Gly
                85   90   95
His Ser Ile Arg Leu Arg His Ala Val Ser Ala Asp Asp Asn Phe Ala
            100   105   110
Thr Leu Thr Gln Val Val Ala Ala Asp Trp Val Glu Ala Glu Gln Leu
        115   120   125
Phe Gly Cys Leu Arg Gln Phe Asn Gly Asp Ile Thr Leu Gln Pro Gly
        130   135   140
Leu Val His Gln Ala Asn Gly Gly Ile Leu Ile Ile Ser Leu Arg Thr
145   150   155   160
Leu Leu Ala Gln Pro Leu Leu Trp Met Arg Leu Lys Asn Ile Val Asn
                165   170   175
Arg Glu Arg Phe Asp Trp Val Ala Phe Asp Glu Ser Arg Pro Leu Pro
            180   185   190
Val Ser Val Pro Ser Met Pro Leu Lys Leu Lys Val Ile Leu Val Gly
        195   200   205
Glu Arg Glu Ser Leu Ala Asp Phe Gln Glu Met Glu Pro Glu Leu Ser
        210   215   220
Glu Gln Ala Ile Tyr Ser Glu Phe Glu Asp Thr Leu Gln Ile Val Asp
225   230   235   240
Ala Glu Ser Val Thr Gln Trp Cys Arg Trp Val Thr Phe Thr Ala Arg
                245   250   255
His Asn His Leu Pro Ala Pro Gly Ala Asp Ala Trp Pro Ile Leu Ile
            260   265   270
Arg Glu Ala Ala Arg Tyr Thr Gly Glu Gln Glu Thr Leu Pro Leu Ser
        275   280   285
Pro Gln Trp Ile Leu Arg Gln Cys Lys Glu Val Ala Ser Leu Cys Asp
        290   295   300

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Gly Asp Thr Phe Ser Gly Glu Gln Leu Asn Leu Met Leu Gln Gln Arg
305   310   315   320

Glu Trp Arg Glu Gly Phe Leu Ala Glu Arg Met Gln Asp Glu Ile Leu
                    325   330   335

Gln Gln Gln Ile Leu Ile Glu Thr Glu Gly Glu Arg Ile Gly Gln Ile
                    340   345   350

Asn Ala Leu Ser Val Ile Glu Phe Pro Gly His Pro Arg Ala Phe Gly
            355   360   365

Glu Pro Ser Arg Ile Ser Cys Val Val His Ile Gly Asp Gly Glu Phe
            370   375   380

Thr Asp Ile Glu Arg Lys Ala Glu Leu Gly Gly Asn Ile His Ala Lys
385   390   395   400

Gly Met Met Ile Met Gln Ala Phe Leu Met Ser Glu Leu Gln Leu Glu
                    405   410   415

Gln Gln Ile Pro Pro Ser Ala Ser Leu Thr Phe Glu Gln Ser Tyr Ser
                    420   425   430

Glu Val Asp Gly Asp Ser Ala Ser Met Ala Glu Leu Cys Ala Leu Ile
            435   440   445

Ser Ala Leu Ala Asp Val Pro Val Asn Gln Ser Ile Ala Ile Thr Gly
            450   455   460

Ser Val Asp Gln Phe Gly Arg Ala Gln Pro Val Gly Gly Leu Asn Glu
465   470   475   480

Lys Ile Glu Gly Phe Phe Ala Ile Lys Gln Gln Arg Glu Leu Thr Gly
                    485   490   495

Lys Gln Gly Val Ile Ile Pro Thr Ala Asn Val Arg His Leu Ser Leu
                    500   505   510

His Ser Glu Leu Val Lys Ala Val Glu Glu Gly Lys Phe Thr Ile Trp
511   515   520

Ala Val Asp Asp Val Thr Asp Ala Leu Pro Leu Leu Leu Asn Leu Val
            530   535   540

Trp Asp Gly Glu Gly Gln Thr Thr Leu Met Gln Thr Ile Gln Glu Arg
545   550   555   560

Ile Ala Gln Ala Ser Gln Gln Glu Gly Arg His Arg Phe Pro Trp Pro
                    565   570   575

Leu Arg Trp Leu Asn Trp Phe Ile Pro Asn
            580   585

    <210> 42
    <211> 584
    <212> PRT
    <213> E. Coli

    <400> 42

Met Ser Lys Glu Lys Phe Glu Arg Thr Lys Pro His Val Asn Val Gly
1   5   10   15

Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
            20   25   30

Thr Thr Val Leu Ala Lys Thr Tyr Gly Gly Ala Ala Arg Ala Phe Asp
            35   40   45

Gln Ile Asp Asn Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
            50   55   60

Thr Ser His Val Glu Tyr Asp Thr Pro Thr Arg His Tyr Ala His Val
65   70   75   80

Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
            85   90   95

Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro

```
                    100                      105                    110
Met Pro Gln Thr Arg Glu His Ile Leu Leu Gly Arg Gln Val Gly Val
               115                   120                    125
Pro Tyr Ile Ile Val Phe Leu Asn Lys Cys Asp Met Val Asp Asp Glu
               130                   145                140
Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ser Gln
145                   150                   155                   160
Tyr Asp Phe Pro Gly Asp Asp Thr Pro Ile Val Arg Gly Ser Ala Leu
                    165                   170                    175
Lys Ala Leu Glu Gly Asp Ala Glu Trp Glu Ala Lys Ile Leu Glu Leu
               180                   185                    190
Ala Gly Phe Leu Asp Ser Tyr Ile Pro Glu Pro Glu Arg Ala Ile Asp
               195                   200                    205
Lys Pro Pro Leu Leu Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg
               210                   215                    220
Gly Thr Val Val Thr Gly Arg Val Glu Arg Gly Ile Ile Lys Val Gly
225                   230                    235                   240
Glu Glu Val Glu Ile Val Gly Ile Lys Glu Thr Gln Lys Ser Thr Cys
                    245                   250                    255
Thr Gly Val Glu Met Phe Arg Lys Leu Leu Asp Glu Gly Arg Ala Gly
               260                   265                    270
Glu Asn Val Gly Val Leu Leu Arg Gly Ile Lys Arg Glu Glu Ile Glu
               275                   280                    285
Arg Gly Gln Val Leu Ala Lys Pro Gly Thr Ile Lys Pro His Thr Lys
               290                   295                300
Phe Glu Ser Glu Val Tyr Ile Leu Ser Lys Asp Glu Gly Gly Arg His
305                   310                    315                   320
Thr Pro Phe Phe Lys Gly Tyr Arg Pro Gln Phe Tyr Phe Arg Thr Thr
               325                   330                    335
Asp Val Thr Gly Thr Ile Glu Leu Pro Glu Gly Val Glu Met Val Met
               340                   345                    350
Pro Gly Asp Asn Ile Lys Met Val Val Thr Leu Ile His Pro Ile Ala
               355                   360                    365
Met Asp Asp Gly Leu Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Val
               370                   375                380
Gly Ala Gly Val Val Ala Lys Val Leu Gly
385                   390
```

```
Met Ala Arg Thr Thr Pro Ile Ala Arg Tyr Arg Asn Ile Gly Ile Ser
1                     5                    10                   15
Ala His Ile Asp Ala Gly Lys Thr Thr Thr Thr Glu Arg Ile Leu Phe
               20                   25                    30
Tyr Thr Gly Val Asn His Lys Ile Gly Glu Val His Arg Gly Ala Ala
               35                   40                   45
Thr Met Asp Trp Met Glu Gln Glu Gln Glu Arg Gly Ile Thr Ile Thr
       50                   55                    60
Ser Ala Ala Thr Thr Ala Phe Trp Ser Gly Met Ala Lys Gln Tyr Glu
65                   70                   75                    80
Pro His Arg Ile Asn Ile Ile Asp Thr Pro Gly His Val Asp Phe Thr
```

```
              85                    90                    95
Ile Glu Val Glu Arg Ser Met Arg Val Leu Asp Gly Ala Val Met Val
              100                   105                   110
Tyr Cys Ala Val Gly Gly Val Gln Pro Gln Ser Glu Thr Val Trp Arg
    115                   120                   125
Gln Ala Asn Lys Tyr Lys Val Pro Arg Ile Ala Phe Val Asn Lys Met
    130                   135                   140
Asp Arg Met Gly Ala Asn Phe Leu Lys Val Val Asn Gln Ile Lys Thr
145                   150                   155                   160
Arg Leu Gly Ala Asn Pro Val Pro Leu Gln Leu Ala Ile Gly Ala Glu
                  165                   170                   175
Glu His Phe Thr Gly Val Val Asp Leu Val Lys Met Lys Ala Ile Asn
              180                   185                   190
Trp Asn Asp Ala Asp Gln Gly Val Thr Phe Glu Tyr Glu Asp Ile Pro
              195                   200                   205
Ala Asp Met Val Glu Leu Ala Asn Glu Trp His Gln Asn Leu Ile Glu
              210                   215                   220
Ser Ala Ala Gln Ala Ser Glu Glu Leu Met Glu Lys Tyr Leu Gly Gly
225                   230                   235                   240
Gln Glu Leu Thr Glu Ala Glu Ile Lys Gly Ala Leu Arg Gln Arg Val
                  245                   250                   255
Leu Asn Asn Gln Ile Ile Leu Val Thr Cys Gly Ser Ala Phe Lys Asn
              260                   265                   270
Lys Gly Val Gln Ala Met Leu Asp Ala Val Ile Asp Tyr Leu Pro Ser
              275                   280                   285
Pro Val Asp Val Pro Ala Ile Asn Gly Ile Leu Asp Asp Gly Lys Asp
              290                   295                   300
Thr Pro Ala Glu Arg His Ala Ser Asp Asp Glu Pro Phe Ser Ala Leu
305                   310                   315                   320
Ala Phe Lys Ile Ala Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe
                  325                   330                   335
Arg Val Tyr Ser Gly Val Val Asn Ser Gly Asp Thr Val Leu Asn Ser
              340                   345                   350
Val Lys Ala Ala Arg Glu Arg Phe Gly Arg Ile Val Gln Met His Ala
              355                   360                   365
Asn Lys Arg Glu Glu Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala
              370                   375                   380
Ala Ile Gly Leu Lys Asp Val Thr Thr Gly Asp Thr Leu Cys Asp Pro
385                   390                   395                   400
Asp Ala Pro Ile Ile Leu Glu Arg Met Glu Phe Pro Glu Pro Val Ile
                  405                   410                   415
Ser Ile Ala Val Glu Pro Lys Thr Lys Ala Asp Gln Glu Lys Met Gly
              420                   425                   430
Leu Ala Leu Gly Arg Leu Ala Lys Glu Asp Pro Ser Phe Arg Val Trp
              435                   440                   445
Thr Asp Glu Glu Ser Asn Gln Thr Ile Ile Ala Gly Met Gly Glu Leu
              450                   455                   460
His Leu Asp Ile Ile Val Asp Arg Met Lys Arg Glu Phe Asn Val Glu
465                   470                   475                   480
Ala Asn Val Gly Lys Pro Gln Val Ala Tyr Arg Glu Thr Ile Arg Gln
                  485                   490                   495
Lys Val Thr Asp Val Glu Gly Lys His Ala Lys Gln Ser Gly Gly Arg
              500                   505                   510
Gly Gln Tyr Gly His Val Val Ile Asp Met Tyr Pro Leu Glu Pro Gly
              515                   520                   525
Ser Asn Pro Lys Gly Tyr Glu Phe Ile Asn Asp Ile Lys Gly Gly Val
              530                   535                   540
```

Ile Pro Gly Glu Tyr Ile Pro Ala Val Asp Lys Gly Ile Gln Glu Gln
545   550   555   560

Leu Lys Ala Gly Pro Leu Ala Gly Tyr Pro Val Val Asp Met Gly Ile
            565   570   575

Arg Leu His Phe Gly Ser Tyr His Asp Val Asp Ser Ser Glu Leu Ala
            580   585   590

Phe Lys Leu Ala Ala Ser Ile Ala Phe Lys Glu Gly Phe Lys Lys Ala
            595   600   605

Lys Pro Val Leu Leu Glu Pro Ile Met Lys Val Glu Val Glu Thr Pro
        610   615   620

Glu Glu Asn Thr Gly Asp Val Ile Gly Asp Leu Ser Arg Arg Arg Gly
625   630   635   640

Met Leu Lys Gly Gln Glu Ser Glu Val Thr Gly Val Lys Ile His Ala
                645   650   655

Glu Val Pro Leu Ser Glu Met Phe Gly Tyr Ala Thr Gln Leu Arg Ser
                660   665   670

Leu Thr Lys Gly Arg Ala Ser Tyr Thr Met Glu Phe Leu Lys Tyr Asp
            675   680   685

Glu Ala Pro Ser Asn Val Ala Gln Ala Val Ile Glu Ala Arg Gly Lys
            690   695   700

        <210> 243
        <211> 178
        <212> PRT
        <213> E. Coli

        <400> 243

Met Pro Arg Arg Val Ile Gly Gln Arg Lys Ile Leu Pro Asp Pro
1   5   10   15

Lys Phe Gly Ser Glu Leu Leu Ala Lys Phe Val Asn Ile Leu Met Val
            20   25   30

Asp Gly Lys Lys Ser Thr Ala Glu Ser Ile Val Tyr Ser Ala Leu Glu
            35   40   45

Thr Leu Ala Gln Arg Ser Gly Lys Ser Glu Leu Glu Ala Phe Glu Val
            50   55   60

Ala Leu Glu Asn Val Arg Pro Thr Val Glu Val Lys Ser Arg Arg Val
65   70   75   80

Gly Gly Ser Thr Tyr Gln Val Pro Val Glu Val Arg Pro Val Arg Arg
                85   90   95

Asn Ala Leu Ala Met Arg Trp Ile Val Glu Ala Ala Arg Lys Arg Gly
                100   105   110

Asp Lys Ser Met Ala Leu Arg Leu Ala Asn Glu Leu Ser Asp Ala Ala
            115   120   125

Glu Asn Lys Gly Thr Ala Val Lys Lys Arg Glu Asp Val His Arg Met
            130   135   140

Ala Glu Ala Asn Lys Ala Phe Ala His Tyr Arg Trp Leu Ser Leu Arg
145   150   155   160

Ser Phe Ser His Gln Ala Gly Ala Ser Ser Lys Gln Pro Ala Leu Gly
                165   170   175

Tyr Leu Asn

        <210> 244
        <211> 134
        <212> PRT

<213> E. Coli

<400> 250

Met Ala Thr Val Asn Gln Leu Val Arg Lys Pro Arg Ala Arg Lys Val
1   5   10   15
Ala Lys Ser Asn Val Pro Ala Leu Glu Ala Cys Pro Gln Lys Arg Gly
                20   25   30
Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala
                35   40   45
Leu Arg Lys Val Cys Arg Val Arg Leu Thr Asn Gly Phe Glu Val Thr
50   55   60
Ser Tyr Ile Gly Gly Glu Gly His Asn Leu Gln Glu His Ser Val Ile
65   70   75   80
Leu Ile Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr His
                    85   90   95
Thr Val Arg Gly Ala Leu Asp Cys Ser Gly Val Lys Asp Arg Lys Gln
                    100   105   110
Ala Asn Ser Lys Tyr Gly Val Lys Arg Pro Lys Ala
                    115   120

<210> ...
<211> ...
<212> PRT
<213> E. Coli

<400> ...

Met Ala Leu Asn Leu Gln Asp Lys Gln Ala Ile Val Ala Glu Val Ser
1   5   10   15
Glu Val Ala Lys Gly Ala Leu Ser Ala Val Val Ala Asp Ser Arg Gly
                20   25   30
Val Thr Val Asp Lys Met Thr Glu Leu Arg Lys Ala Gly Arg Glu Ala
                35   40   45
Gly Val Tyr Met Arg Val Val Arg Asn Thr Leu Leu Arg Arg Ala Val
50   55   60
Glu Gly Thr Pro Phe Glu Cys Leu Lys Asp Ala Phe Val Gly Pro Thr
65   70   75   80
Leu Ile Ala Tyr Ser Met Glu His Pro Gly Ala Ala Ala Arg Leu Phe
                    85   90   95
Lys Gln Phe Ala Lys Ala Asn Ala Lys Phe Glu Val Lys Ala Ala Ala
                    100   105   110
Phe Gln Gly Glu Leu Ile Pro Ala Ser Gln Ile Asp Arg Leu Ala Thr
                    115   120   125
Leu Pro Thr Tyr Glu Glu Ala Ile Ala Arg Leu Met Ala Thr Met Lys
     130   135   140
Glu Ala Ser Ala Gly Lys Leu Val Arg Thr Leu Ala Ala Val Arg Asp
145   150   155   160
Ala Lys Gln Ala Ala
                    165

<210> ...
<211> 111
<212> PRT
<213> E. Coli

<400> 252

Met Ser Ile Thr Lys Asp Gln Ile Ile Glu Ala Val Ala Ala Met Ser
1   5   10   15

Val Met Asp Val Val Glu Leu Ile Ser Ala Met Glu Glu Lys Phe Gly
         20   25   30

Val Ser Ala Ala Ala Ala Val Ala Val Ala Ala Gly Pro Val Glu Ala
         35   40   45

Ala Glu Glu Lys Thr Glu Phe Asp Val Ile Leu Lys Ala Ala Gly Ala
         50   55   60

Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly Leu Gly
65   70   75   80

Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Ala Leu Lys
         85   90   95

Glu Gly Val Ser Lys Asp Asp Ala Glu Ala Leu Lys Lys Ala Leu Glu
         100   105   110

Glu Ala Gly Ala Glu Val Glu Val Lys
         115   120

        (2)   A-3
        (2)   T14
        (2)   Pkf
        (2)   E. Coli

        (4)   2-3

Met Ser Arg Ile Ile Met Leu Ile Pro Thr Gly Thr Ser Val Gly Leu
1   5   10   15

Thr Ser Val Ser Leu Gly Val Ile Arg Ala Met Glu Arg Lys Gly Val
         20   25   30

Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp
         35   40   45

Ala Pro Asp Gln Thr Thr Thr Ile Val Arg Ala Asn Ser Ser Thr Thr
         50   55   60

Thr Ala Ala Glu Pro Leu Lys Met Ser Tyr Val Glu Gly Leu Leu Ser
65   70   75   80

Ser Asn Gln Lys Asp Val Leu Met Glu Glu Ile Val Ala Asn Tyr His
         85   90   95

Ala Asn Thr Lys Asp Ala Glu Val Val Leu Val Glu Gly Leu Val Pro
         100   105   110

Thr Arg Lys His Gln Phe Ala Gln Ser Leu Asn Tyr Glu Ile Ala Lys
         115   120   125

Thr Leu Asn Ala Glu Ile Val Phe Val Met Ser Gln Gly Thr Asp Thr
         130   135   140

Pro Glu Gln Leu Lys Glu Arg Ile Glu Leu Thr Arg Asn Ser Phe Gly
145   150   155   160

Gly Ala Lys Asn Thr Asn Ile Thr Gly Val Ile Val Asn Lys Leu Asn
         165   170   175

Ala Pro Val Asp Glu Gln Gly Arg Thr Arg Pro Asp Leu Ser Glu Ile
         180   185   190

Phe Asp Asp Ser Ser Lys Ala Lys Val Asn Asn Val Asp Pro Ala Lys
         195   200   205

Leu Gln Gln Ser Ser Pro Leu Pro Val Leu Gly Ala Val Pro Trp Ser
         210   215   220

Phe Asp Leu Ile Ala Thr Arg Ala Ile Asp Met Ala Arg His Leu Asn
125   230   235   240

Ala Thr Ile Ile Asn Glu Gly Asp Ile Asn Thr Arg Arg Val Lys Ser
         245   250   255

Val Thr Phe Cys Ala Arg Ser Ile Pro His Met Leu Glu His Phe Arg

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                    260                      265                      270
Ala Gly Ser Leu Leu Val Thr Ser Ala Asp Arg Pro Asp Val Leu Val
                    275                      280                      285
Ala Ala Cys Leu Ala Ala Met Asn Gly Val Glu Ile Gly Ala Leu Leu
        291                      295                      300
Leu Thr Gly Gly Tyr Glu Met Asp Ala Arg Ile Ser Lys Leu Cys Glu
305                      310                      315                      320
Arg Ala Phe Ala Thr Gly Leu Pro Val Phe Met Val Asn Thr Asn Thr
                    325                      330                      335
Trp Gln Thr Ser Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val
                    340                      345                      350
Asp Asp His Glu Arg Ile Glu Lys Val Gln Glu Tyr Val Ala Asn Tyr
        355                      360                      365
Ile Asn Ala Asp Trp Ile Glu Ser Leu Thr Ala Thr Ser Glu Arg Ser
        371                      375                      380
Arg Arg Leu Ser Pro Arg Ala Phe Arg Tyr Gln Leu Thr Glu Leu Ala
386                      390                      395                      400
Arg Lys Ala Gly Lys Arg Ile Val Leu Pro Glu Gly Asp Glu Pro Arg
                    405                      410                      415
Thr Val Lys Ala Ala Ala Ile Cys Ala Glu Arg Gly Ile Ala Thr Cys
        420                      425                      430
Val Leu Leu Gly Asn Pro Ala Glu Ile Asn Arg Val Ala Ala Ser Gln
        435                      440                      445
Gly Val Glu Leu Gly Ala Gly Ile Glu Ile Val Asp Pro Glu Val Val
        450                      455                      460
Arg Glu Ser Tyr Val Gly Arg Leu Val Glu Leu Arg Lys Asn Lys Gly
465                      470                      475                      480
Met Thr Glu Thr Val Ala Arg Glu Gln Leu Glu Asp Asn Val Val Leu
                    485                      490                      495
Gly Thr Leu Met Leu Glu Gln Asp Glu Val Asp Gly Leu Val Ser Gly
                    500                      505                      510
Ala Val His Thr Thr Ala Asn Thr Ile Arg Pro Pro Leu Gln Leu Ile
        515                      520                      525
Lys Thr Ala Pro Gly Ser Ser Leu Val Ser Ser Val Phe Phe Met Leu
        531                      535                      540
Leu Pro Glu Gln Val Tyr Val Tyr Gly Asp Cys Ala Ile Asn Pro Asp
545                      550                      555                      560
Pro Thr Ala Glu Gln Leu Ala Glu Ile Ala Ile Gln Ser Ala Asp Ser
                    565                      570                      575
Ala Ala Ala Pro Gly Ile Glu Pro Arg Val Ala Met Leu Ser Tyr Ser
        561                      565                      590
Thr Gly Thr Ser Gly Ala Gly Ser Asp Val Glu Lys Val Arg Glu Ala
        595                      600                      605
Thr Arg Leu Ala Gln Glu Lys Arg Pro Asp Leu Met Ile Asp Gly Pro
        610                      615                      620
Leu Gln Tyr Asp Ala Ala Val Met Ala Asp Val Ala Lys Ser Lys Ala
625                      630                      635                      640
Pro Asn Ser Pro Val Ala Gly Arg Ala Thr Val Phe Ile Phe Pro Asp
                    645                      650                      655
Leu Asn Thr Gly Asn Thr Thr Tyr Lys Ala Val Gln Arg Ser Ala Asp
        660                      665                      670
Leu Ile Ser Ile Gly Pro Met Leu Gln Gly Met Arg Lys Pro Val Asn
        675                      680                      685
Asp Leu Ser Arg Gly Ala Leu Val Asp Asp Ile Val Tyr Thr Ile Ala
        690                      695                      700
Leu Thr Ala Ile Gln Ser Ala Gln Gln Gln
705                      710
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<210> 154
<211> 583
<212> PRT
<213> E. Coli

<400> 154

Met Asn Asn Ser Ile Asn His Lys Phe His His Ile Ser Arg Ala Glu
1   5   10   15

Tyr Gln Glu Leu Leu Ala Val Ser Arg Gly Asp Ala Val Ala Asp Tyr
            20   25   30

Ile Ile Asp Asn Val Ser Ile Leu Asp Leu Ile Asn Gly Gly Glu Ile
            35   40   45

Ser Gly Pro Ile Val Ile Lys Gly Arg Tyr Ile Ala Gly Val Gly Ala
        50   55   60

Glu Tyr Thr Asp Ala Pro Ala Leu Gln Arg Ile Asp Ala Arg Gly Ala
65   70   75   80

Thr Ala Val Pro Gly Phe Ile Asp Ala His Leu His Ile Glu Ser Ser
            85   90   95

Met Met Thr Pro Val Thr Phe Glu Thr Ala Thr Leu Pro Arg Gly Leu
            100   105   110

Thr Thr Val Ile Cys Asp Pro His Glu Ile Val Asn Val Met Gly Glu
            115   120   125

Ala Gly Phe Ala Trp Phe Ala Arg Cys Ala Glu Gln Ala Arg Gln Asn
        130   135   140

Gln Tyr Leu Ala Val Ser Ser Cys Val Pro Ala Leu Glu Gly Cys Asp
145   150   155   160

Val Asn Gly Ala Ser Phe Thr Leu Glu Gln Met Leu Ala Trp Arg Asp
                165   170   175

Ile Ser Gly Gln Asn Ala Leu Leu Asp Lys Leu Asp Ala Phe Arg His
            180   185   190

Leu Thr Leu Asp Gly His Cys Pro Gly Leu Gly Gly Lys Glu Leu Asn
            195   200   205

Ala Tyr Ile Thr Ala Gly Ile Glu Asn Cys His Glu Ser Tyr Gln Leu
125   250   255   310

Glu Glu Gly Arg Arg Lys Leu Gln Leu Gly Met Ser Leu Met Ile Arg
            245   250   255

Glu Gly Ser Ala Ala Arg Asn Leu Asn Ala Leu Ala Pro Leu Ile Asn
            260   265   270

Glu Phe Asn Ser Pro Gln Cys Met Leu Cys Thr Asp Asp Arg Asn Pro
            275   280   285

Trp Glu Ile Ala His Glu Gly His Ile Asp Ala Leu Ile Arg Arg Leu
            290   295   300

Ile Glu Gln His Asn Val Pro Leu His Val Ala Tyr Arg Val Ala Ser
305   310   315   320

Trp Ser Thr Ala Arg His Phe Gly Leu Asn His Leu Gly Leu Leu Ala
            325   330   335

Pro Gly Lys Gln Ala Asp Ile Val Leu Leu Ser Asp Ala Arg Lys Val
            340   345   350

Thr Val Gln Gln Val Leu Val Lys Gly Glu Pro Ile Asp Ala Gln Thr
            355   360   365

Leu Gln Ala Glu Glu Ser Ala Arg Leu Ala Gln Ser Ala Pro Pro Tyr
            370   375   380

Gly Asn Thr Ile Ala Arg Gln Pro Val Ser Ala Ser Asp Phe Ala Leu

385   390   395   400

Gln Phe Thr Pro Gly Lys Arg Tyr Arg Val Ile Asp Val Ile His Asn

           405   410   415

Glu Leu Ile Thr His Ser His Ser Ser Val Tyr Ser Glu Asn Gly Phe

           420   425   430

Asp Arg Asp Asp Val Ser Phe Ile Ala Val Leu Glu Arg Tyr Gly Gln

           435   440   445

Arg Leu Ala Pro Ala Cys Gly Leu Leu Gly Gly Phe Gly Leu Asn Glu

  465   470   475   480

Gly Ala Leu Ala Ala Thr Val Ser His Asp Ser His Asn Ile Val Val

           485   490   495

Ile Gly Arg Ser Ala Glu Glu Met Ala Leu Ala Val Asn Gln Val Ile

Gln Asp Gly Gly Gly Leu Cys Val Val Arg Asn Gly Gln Val Gln Ser

           500   505   510

His Leu Pro Leu Pro Ile Ala Gly Leu Met Ser Thr Asp Thr Ala Gln

           515   520   525

Ser Leu Ala Glu Gln Ile Asp Ala Leu Lys Ala Ala Ala Arg Gln Cys

           530   535   540

Gly Pro Leu Pro Asp Glu Pro Phe Ile Gln Met Ala Phe Leu Ser Leu

545   550   555   560

Pro Val Ile Pro Ala Leu Lys Leu Thr Ser Gln Gly Leu Phe Asp Gly

           565   570   575

Glu Lys Pro Ala Phe Thr Thr Leu Glu Val Thr Glu

           580   585

<210> 155
<211> 405
<212> PRT
<213> E. Coli

<400> 155

Met Ala Tyr Cys Asn Pro Gly Leu Glu Ser Arg Pro Asn Lys Arg Asn
 1   5   10   15

Ala Leu Arg Arg His Val Val Thr Gly Ile Gly Met Lys Ile Val Ile
          20   25   30

Ala Pro Asp Ser Tyr Lys Glu Ser Leu Ser Ala Ser Glu Val Ala Gln
          35   40   45

Ala Ile Glu Lys Gly Phe Arg Glu Ile Phe Pro Asp Ala Gln Tyr Val
          50   55   60

Ser Val Pro Val Ala Asp Gly Gly Glu Gly Thr Val Glu Ala Met Ile
65   70   75   80

Ala Ala Thr Gln Gly Ala Glu Arg His Ala Trp Val Thr Gly Pro Leu
          85   90   95

Gly Glu Lys Val Asn Ala Ser Trp Gly Ile Ser Gly Asp Gly Lys Thr
          100   105   110

Ala Phe Ile Glu Met Ala Ala Ala Ser Gly Leu Glu Leu Val Pro Ala
          115   120   125

Glu Lys Arg Asp Pro Leu Val Thr Thr Ser Arg Gly Thr Gly Glu Leu
          130   135   140

Ile Leu Glu Ala Leu Glu Ser Gly Ala Thr Asn Ile Ile Ile Gly Ile
          145   150   155   160

Gly Gly Ser Ala Thr Asn Asp Gly Gly Ala Gly Met Val Gln Ala Leu
                165   170   175

Gly Ala Lys Leu Cys Asp Ala Asn Gly Asn Glu Ile Gly Phe Gly Gly
          180   185   190

Gly Ser Leu Asn Thr Leu Asn Asp Ile Asp Ile Ser Gly Leu Asp Pro
            195   200   205

Arg Leu Lys Asp Cys Val Ile Arg Val Ala Cys Asp Val Thr Asn Pro
    210   215   220

Leu Val Gly Asp Asn Gly Ala Ser Arg Ile Phe Gly Pro Gln Lys Gly
225   230   235   240

Ala Ser Glu Ala Met Ile Val Glu Leu Asp Asn Asn Leu Ser His Tyr
            245   250   255

Ala Glu Val Ile Lys Lys Ala Leu His Val Asp Val Lys Asp Val Pro
            260   265   270

Gly Ala Gly Ala Ala Gly Gly Met Gly Ala Ala Leu Met Ala Phe Leu
    275   280   285

Gly Ala Glu Leu Lys Ser Gly Ile Glu Ile Val Thr Thr Ala Leu Asn
    290   295   300

Leu Glu Glu His Ile His Asp Lys Thr Leu Val Ile Thr Gly Glu Gly
305   310   315   320

Arg Ile Asp Ser Gln Ser Ile His Gly Lys Val Pro Ile Gly Val Ala
            325   330   335

Asn Val Ala Lys Lys Tyr His Lys Pro Val Ile Gly Ile Ala Gly Ser
            340   345   350

Leu Thr Asp Asp Val Gly Val Val His Gln His Gly Ile Asp Ala Val
        355   360   365

Phe Ser Val Leu Thr Ser Ile Gly Thr Leu Asp Glu Ala Phe Arg Gly
    370   375   380

Ala Tyr Asp Asn Ile Cys Arg Ala Ser Arg Asn Ile Ala Ala Thr Leu
385   390   395   400

Ala Ile Gly Met Arg Asn Ala Gly
            405

    <210> 166
    <211> 439
    <212> PRT
    <213> E. Coli

    <400> 166

Met Ile Asp Met Thr Met Lys Val Gly Phe Ile Gly Leu Gly Ile Met
1   5   10   15

Gly Lys Pro Met Ser Lys Asn Leu Leu Lys Ala Gly Tyr Ser Leu Val
            20   25   30

Val Ala Asp Arg Asn Pro Glu Ala Ile Ala Asp Val Ile Ala Ala Gly
        35   40   45

Ala Glu Thr Ala Ser Thr Ala Lys Ala Ile Ala Glu Gln Cys Asp Val
    51   55   60

Ile Ile Thr Met Leu Pro Asn Ser Pro His Val Lys Glu Val Ala Leu
65   70   75   80

Gly Glu Asn Gly Ile Ile Glu Gly Ala Lys Pro Gly Thr Val Leu Ile
                85   90   95

Asp Met Ser Ser Ile Ala Pro Leu Ala Ser Arg Glu Ile Ser Glu Ala
            100   105   110

Leu Lys Ala Lys Gly Ile Asp Met Leu Asp Ala Pro Val Ser Gly Gly
    117   120   125

Gln Pro Lys Ala Ile Asp Gly Thr Leu Ser Val Met Val Gly Gly Asp
    130   135   140

Lys Ala Ile Phe Asp Lys Tyr Tyr Asp Leu Met Lys Ala Met Ala Gly
145   150   155   160

Ser Val Val His Thr Gly Glu Ile Gly Ala Gly Asn Val Thr Lys Leu

```
                       165                     170                     175
Ala Asn Gln Val Ile Val Ala Leu Asn Ile Ala Ala Met Ser Glu Ala
                       180                     185                     190
Leu Thr Leu Ala Thr Lys Ala Gly Val Asn Pro Asp Leu Val Tyr Gln
                       195                     200                     205
Ala Ile Arg Gly Gly Leu Ala Gly Ser Thr Val Leu Asp Ala Lys Ala
             210                     215                     220
Pro Met Val Met Asp Arg Asn Phe Lys Pro Gly Phe Arg Ile Asp Leu
                       225                     230                     235                     240
His Ile Lys Asp Leu Ala Asn Ala Leu Asp Thr Ser His Gly Val Gly
                       245                     250                     255
Ala Gln Leu Pro Leu Thr Ala Ala Val Met Glu Met Met Gln Ala Leu
                       260                     265                     270
Arg Ala Asp Gly Leu Gly Thr Ala Asp His Ser Ala Leu Ala Cys Tyr
                       275                     280                     285
Tyr Glu Lys Leu Ala Lys Val Glu Val Thr Arg
             290                     295
```

<211> ...
<211> ...
<211> PRT
<213> E. Coli

<400> 257

```
Met Asn Asn Asp Val Phe Pro Asn Lys Phe Lys Ala Ala Leu Ala Ala
  1                   5                    10                    15
Lys Gln Val Gln Ile Gly Cys Trp Ser Ala Leu Ser Asn Pro Ile Ser
             20                    25                    30
Thr Glu Val Leu Gly Leu Ala Gly Phe Asp Trp Leu Val Leu Asp Gly
             35                    40                    45
Glu His Ala Pro Asn Asp Ile Ser Thr Phe Ile Pro Gln Leu Met Ala
             50                    55                    60
Leu Lys Gly Ser Ala Ser Ala Pro Val Val Arg Val Pro Thr Asn Glu
 65                    70                    75                    80
Pro Val Ile Ile Lys Arg Leu Leu Asp Ile Gly Phe Tyr Asn Phe Leu
                   85                    90                    95
Ile Pro Phe Val Glu Thr Lys Glu Glu Ala Glu Leu Ala Val Ala Ser
                  100                   105                   110
Thr Arg Tyr Pro Pro Glu Gly Ile Arg Gly Val Ser Val Ser His Arg
                  115                   120                   125
Ala Asn Met Phe Gly Thr Val Ala Asp Tyr Phe Ala Gln Ser Asn Lys
             130                   135                   140
Asn Ile Thr Ile Leu Val Gln Ile Glu Ser Gln Gln Gly Val Asp Asn
 145                   150                   155                   160
Val Asp Ala Ile Ala Ala Thr Glu Gly Val Asp Gly Ile Phe Val Gly
                  165                   170                   175
Pro Ser Asp Leu Ala Ala Ala Leu Gly His Leu Gly Asn Ala Ser His
             180                   185                   190
Pro Asp Val Gln Lys Ala Ile Gln His Ile Phe Asn Arg Ala Ser Ala
             195                   200                   205
His Gly Lys Pro Ser Gly Ile Leu Ala Pro Val Glu Ala Asp Ala Arg
             210                   215                   220
Arg Tyr Leu Glu Trp Gly Ala Thr Phe Val Ala Val Gly Ser Asp Leu
 225                   230                   235                   240
Gly Val Phe Arg Ser Ala Thr Gln Lys Leu Ala Asp Thr Phe Lys Lys
```

245　　　　　　250　　　　　　255

<210> 253
<211> 444
<212> PRT
<213> E. Coli

<400> 253

```
Met Ile Leu Asp Thr Val Asp Glu Lys Lys Lys Gly Val His Thr Arg
1                   5                   10                  15
Tyr Leu Ile Leu Leu Ile Ile Phe Ile Val Thr Ala Val Asn Tyr Ala
                20                                  30
Asp Arg Ala Thr Leu Ser Ile Ala Gly Thr Glu Val Ala Lys Glu Leu
        35                  40                  45
Gln Leu Ser Ala Val Ser Met Gly Tyr Ile Phe Ser Ala Phe Gly Trp
    50                  55                  60
Ala Tyr Leu Leu Met Gln Ile Pro Gly Gly Trp Leu Leu Asp Lys Phe
65                  70                  75                  80
Gly Ser Lys Lys Val Tyr Thr Tyr Ser Leu Phe Phe Trp Ser Leu Pro
                85                  90                  95
Thr Phe Leu Gln Gly Phe Val Asp Met Phe Pro Leu Ala Trp Ala Gly
                100                 105                 110
Ile Ser Met Phe Phe Met Arg Phe Met Leu Gly Phe Ser Glu Ala Pro
        115                 120                 125
Ser Phe Pro Ala Asn Ala Arg Ile Val Ala Ala Trp Phe Pro Thr Lys
    130                 135                 140
Glu Arg Gly Thr Ala Ser Ala Ile Phe Asn Ser Ala Gln Tyr Phe Ser
145                 150                 155                 160
Leu Ala Leu Phe Ser Pro Leu Leu Gly Trp Leu Thr Phe Ala Trp Gly
                165                 170                 175
Trp Gln His Val Phe Thr Val Met Gly Val Ile Gly Phe Val Leu Thr
                180                 185                 190
Ala Leu Trp Ile Lys Leu Ile His Asn Pro Thr Asp His Pro Arg Met
        195                 200                 205
Ser Ala Glu Glu Leu Lys Phe Ile Ser Glu Asn Gly Ala Val Val Asp
        211                 215                 220
Met Asp His Lys Lys Pro Gly Ser Ala Ala Ala Ser Gly Pro Lys Leu
    225                 230                 235                 240
His Tyr Ile Lys Gln Leu Leu Ser Asn Arg Met Met Leu Gly Val Pro
                245                 250                 255
Phe Gly Gln Tyr Phe Ile Asn Thr Ile Thr Trp Phe Phe Leu Thr Trp
            260                 265                 270
Phe Pro Ile Tyr Leu Val Gln Glu Lys Gly Met Ser Ile Leu Lys Val
        275                 280                 285
Gly Leu Val Ala Ser Ile Pro Ala Leu Cys Gly Phe Ala Gly Gly Val
        290                 295                 300
Leu Gly Gly Val Phe Ser Asp Tyr Leu Ile Lys Arg Gly Leu Ser Leu
405                 310                 315                 320
Thr Leu Ala Arg Lys Leu Pro Ile Val Leu Gly Met Leu Leu Ala Ser
                325                 330                 335
Thr Ile Ile Leu Cys Asn Tyr Thr Asn Asn Thr Thr Leu Val Val Met
            340                 345                 350
Leu Met Ala Leu Ala Phe Phe Gly Lys Gly Phe Gly Ala Leu Gly Trp
        355                 360                 365
Pro Val Ile Ser Asp Thr Ala Pro Lys Glu Ile Val Gly Leu Cys Gly
    370                 375                 380
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```
Gly Val Phe Asn Val Phe Gly Asn Val Ala Ser Ile Val Thr Pro Leu
385                 390                 395                 400
Val Ile Gly Tyr Leu Val Ser Glu Leu His Ser Phe Asn Ala Ala Leu
                405                 410                 415
Val Phe Val Gly Cys Ser Ala Leu Met Ala Met Val Cys Tyr Leu Phe
                420                 425                 430
Val Val Gly Asp Ile Lys Arg Met Glu Leu Gln Lys
                435                 440


    <210> 254
    <211> 511
    <212> PRT
    <213> E. Coli


    <400> 254
Met Gln Thr Ser Asp Thr Arg Ala Leu Pro Leu Leu Cys Ala Arg Ser
1                   5                   10                  15
Val Tyr Lys Gln Tyr Ser Gly Val Asn Val Leu Lys Gly Ile Asp Phe
                20                  25                  30
Thr Leu His Gln Gly Glu Val His Ala Leu Leu Gly Gly Asn Gly Ala
                35                  40                  45
Gly Lys Ser Thr Leu Met Lys Ile Ile Ala Gly Ile Thr Pro Ala Asp
                50                  55                  60
Ser Gly Thr Leu Glu Ile Gly Gly Asn Asn Tyr Val Arg Leu Thr Pro
65                  70                  75                  80
Val His Ala His Gln Leu Gly Ile Tyr Leu Val Pro Gln Glu Pro Leu
                85                  90                  95
Leu Phe Pro Ser Leu Ser Ile Lys Glu Asn Ile Leu Phe Gly Leu Ala
                100                 105                 110
Lys Lys Gln Leu Ser Met Gln Lys Met Lys Asn Leu Leu Ala Ala Leu
                115                 120                 125
Gly Cys Gln Phe Asp Leu His Ser Leu Ala Gly Ser Leu Asp Val Ala
                130                 135                 140
Asp Arg Gln Met Val Glu Ile Leu Arg Gly Leu Met Arg Asp Ser Arg
141                 150                 155                 160
Ile Leu Ile Leu Asp Glu Pro Thr Ala Ser Leu Thr Pro Ala Glu Thr
                165                 170                 175
Glu Arg Leu Pro Ser Arg Leu Gln Glu Leu Leu Ala Thr Gly Val Gly
                180                 185                 190
Ile Val Phe Ile Ser His Lys Leu Pro Glu Ile Arg Gln Ile Ala Asp
                195                 200                 205
Arg Ile Ser Val Met Arg Asp Gly Thr Ile Ala Leu Ser Gly Lys Thr
                210                 215                 220
Ser Glu Leu Ser Thr Asp Asp Ile Ile Gln Ala Ile Thr Pro Ala Val
225                 230                 235                 240
Arg Glu Lys Ser Leu Ser Ala Ser Gln Lys Leu Trp Leu Glu Leu Pro
                245                 250                 255
Gly Asn Arg Pro Gln His Ala Ala Gly Thr Pro Val Leu Thr Leu Glu
                260                 265                 270
Asn Leu Thr Gly Glu Gly Phe Arg Asn Val Ser Leu Thr Leu Asn Ala
                275                 280                 285
Gly Glu Ile Leu Gly Leu Ala Gly Leu Val Gly Ala Gly Arg Thr Glu
                290                 295                 300
Met Ala Glu Thr Leu Tyr Gly Leu Arg Thr Leu Arg Gly Gly Arg Ile
305                 310                 315                 320
Met Leu Asn Gly Lys Glu Ile Asn Lys Leu Ser Thr Gly Glu Arg Leu
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                    325                     330                     335
Leu Arg Gly Leu Val Tyr Leu Pro Glu Asp Arg Gln Ser Ser Gly Leu
            340                     345                     350
Asn Leu Asp Ala Ser Leu Ala Trp Asn Val Cys Ala Leu Thr His Asn
            355                     360                     365
Leu Arg Gly Phe Trp Ala Lys Thr Ala Lys Asp Asn Ala Thr Leu Glu
    370                     375                     380
Arg Tyr Arg Arg Ala Leu Asn Ile Lys Phe Asn Gln Pro Glu Gln Ala
385                     390                     395                     400
Ala Arg Thr Leu Ser Gly Gly Asn Gln Gln Lys Ile Leu Ile Ala Lys
                    405                     410                     415
Cys Leu Glu Ala Ser Pro Gln Val Leu Ile Val Asp Glu Pro Thr Arg
            420                     425                     430
Gly Val Asp Val Ser Ala Arg Asn Asp Ile Tyr Gln Leu Leu Arg Ser
            435                     440                     445
Ile Ala Ala Gln Asn Val Ala Val Leu Leu Ile Ser Ser Asp Leu Glu
    450                     455                     460
Glu Ile Glu Leu Met Ala Asp Arg Val Tyr Val Met His Gln Gly Glu
465                     470                     475                     480
Ile Thr His Ser Ala Leu Thr Glu Arg Asp Ile Asn Val Glu Thr Ile
                    485                     490                     495
Met Arg Val Ala Phe Gly Asp Ser Gln Arg Gln Glu Ala Ser Cys
            500                     505                     510
```

```
Met Leu Lys Phe Ile Gln Asn Asn Arg Glu Ile Thr Ala Leu Leu Ala
1                       5                       10                      15
Val Val Leu Leu Phe Val Leu Pro Gly Phe Leu Asp Arg Gln Tyr Leu
            20                      25                      30
Ser Val Gln Thr Leu Thr Met Val Tyr Ser Ser Ala Gln Ile Leu Ile
            35                      40                      45
Leu Leu Ala Met Gly Ala Thr Leu Val Met Leu Thr Arg Asn Ile Asp
    50                      55                      60
Val Ser Val Gly Ser Ile Thr Gly Met Cys Ala Val Leu Leu Gly Met
63                      70                      75                      80
Leu Leu Asn Ala Gly Tyr Ser Leu Pro Val Ala Cys Val Ala Thr Leu
                    85                      90                      95
Leu Leu Gly Leu Leu Ala Gly Phe Phe Asn Gly Val Leu Val Ala Trp
            100                     105                     110
Leu Lys Ile Pro Ala Ile Val Ala Thr Leu Gly Thr Leu Gly Leu Tyr
            115                     120                     125
Arg Gly Ile Met Leu Leu Trp Thr Gly Gly Lys Trp Ile Glu Gly Leu
    130                     135                     140
Pro Ala Glu Leu Lys Gln Leu Ser Ala Pro Leu Leu Leu Gly Val Ser
145                     150                     155                     160
Ala Ile Gly Trp Leu Thr Ile Ile Leu Val Ala Phe Met Ala Trp Leu
                    165                     170                     175
Leu Ala Lys Thr Ala Phe Gly Arg Ser Phe Tyr Ala Thr Gly Asp Asn
            180                     185                     190
Leu Gln Gly Ala Arg Gln Leu Gly Val Arg Thr Glu Ala Ile Arg Ile
            195                     200                     205
```

Val Ala Phe Ser Leu Asn Gly Cys Met Ala Ala Leu Ala Gly Ile Val
210   215   220

Phe Ala Ser Gln Ile Gly Phe Ile Pro Asn Gln Thr Gly Thr Gly Leu
225   230   235   240

Glu Met Lys Ala Ile Ala Ala Cys Val Leu Gly Gly Ile Ser Leu Leu
                    245   250   255

Gly Gly Ser Gly Ala Ile Ile Gly Ala Val Leu Gly Ala Trp Phe Leu
                260   265   270

Thr Gln Ile Asp Ser Val Leu Val Leu Leu Arg Ile Pro Ala Trp Trp
            275   280   285

Asn Asp Phe Ile Ala Gly Leu Val Leu Leu Ala Val Leu Val Phe Asp
        290   295   300

Gly Arg Leu Arg Cys Ala Leu Glu Arg Asn Leu Arg Arg Gln Lys Tyr
305   310   315   320

Ala Arg Phe Met Thr Pro Pro Pro Ser Val Lys Pro Ala Ser Ser Gly
                325   330   335

Lys Lys Arg Glu Ala Ala
            340

    <210> 201
    <211> 330
    <212> PRT
    <213> E. Coli

    <400> 201

Met Arg Ile Arg Tyr Gly Trp Glu Leu Ala Leu Ala Ala Leu Leu Val
1   5   10   15

Ile Gly Ile Val Ala Phe Gly Ala Ile Asn Pro Arg Met Leu Asp Leu
                    20   25   30

Asn Met Leu Leu Phe Ser Thr Ser Asp Phe Ile Cys Ile Gly Ile Val
            35   40   45

Ala Leu Pro Leu Thr Met Val Ile Val Ser Gly Gly Ile Asp Ile Ser
        50   55   60

Phe Gly Ser Thr Ile Gly Leu Cys Ala Ile Ala Leu Gly Val Leu Pro
65   70   75   80

Gln Ser Gly Val Pro Met Pro Leu Ala Ile Leu Leu Thr Leu Leu Leu
                    85   90   95

Gly Ala Leu Cys Gly Leu Ile Asn Ala Gly Leu Ile Ile Tyr Thr Lys
                100   105   110

Val Asn Pro Leu Val Ile Thr Leu Gly Thr Leu Tyr Leu Phe Ala Gly
            115   120   125

Ser Ala Leu Leu Leu Ser Gly Met Ala Gly Ala Thr Gly Tyr Glu Gly
        130   135   140

Ile Gly Gly Phe Pro Met Ala Phe Thr Asp Phe Ala Asn Leu Asp Val
145   150   155   160

Leu Gly Leu Pro Val Pro Leu Ile Ile Phe Leu Ile Cys Leu Leu Val
                165   170   175

Phe Trp Leu Trp Leu His Lys Thr His Ala Gly Arg Asn Val Phe Leu
                180   185   190

Ile Gly Gln Ser Pro Arg Val Ala Leu Tyr Ser Ala Ile Pro Val Asn
            190   200   205

Arg Thr Leu Cys Ala Leu Tyr Ala Met Thr Gly Leu Ala Ser Ala Val
        210   215   220

Ala Ala Val Leu Leu Val Ser Tyr Phe Gly Ser Ala Arg Ser Asp Leu
225   230   235   240

Gly Ala Ser Phe Leu Met Pro Ala Ile Thr Ala Val Val Leu Gly Gly
                245   250   255

Ala Asn Ile Tyr Gly Gly Ser Gly Ser Ile Ile Gly Thr Ala Ile Ala
        260   265   270

Val Leu Leu Val Gly Tyr Leu Gln Gln Gly Leu Gln Met Ala Gly Val
     275   280   285

Pro Asn Gln Val Ser Ser Ala Leu Ser Gly Ala Leu Leu Ile Val Val
    290   295   300

Val Val Gly Arg Ser Val Ser Leu His Arg Gln Gln Ile Lys Glu Trp
  305   310   315   320

Leu Ala Arg Arg Ala Asn Asn Pro Leu Pro
       315   330

<210> 26?
<211> 34?
<212> PRT
<213> E. Coli

<400> 26?

Met Thr Leu His Arg Phe Lys Lys Ile Ala Leu Leu Ser Ala Leu Gly
 1   5   10   15

Ile Ala Ala Ile Ser Met Asn Val Gln Ala Ala Glu Arg Ile Ala Phe
                  20   30

Ile Pro Lys Leu Val Gly Val Gly Phe Phe Thr Ser Gly Gly Asn Gly
     35   40   45

Ala Gln Gln Ala Gly Lys Glu Leu Gly Val Asp Val Thr Tyr Asp Gly
    50   55   60

Pro Thr Glu Pro Ser Val Ser Gly Gln Val Gln Leu Ile Asn Asn Phe
65   70   75   80

Val Asn Gln Gly Tyr Asn Ala Ile Ile Val Ser Ala Val Ser Pro Asp
          85   90   95

Gly Leu Cys Pro Ala Leu Lys Arg Ala Met Gln Arg Gly Val Arg Val
          100   105   110

Leu Thr Trp Asp Ser Asp Thr Lys Pro Glu Cys Arg Ser Tyr Tyr Ile
     115   120   125

Asn Gln Gly Thr Pro Ala Gln Leu Gly Gly Met Leu Val Asp Met Ala
  130   135   140

Ala Arg Gln Val Asn Lys Asp Lys Ala Lys Val Ala Phe Phe Tyr Ser
145   150   155   160

Ser Pro Thr Val Thr Asp Gln Asn Gln Trp Val Lys Glu Ala Lys Ala
          165   170   175

Lys Ile Ala Lys Glu His Pro Gly Trp Glu Ile Val Thr Thr Gln Phe
         180   185   190

Gly Tyr Asn Asp Ala Thr Lys Ser Leu Gln Thr Ala Glu Gly Ile Leu
     195   200   205

Lys Ala Tyr Ser Asp Leu Asp Ala Ile Ile Ala Pro Asp Ala Asn Ala
  210   215   220

Leu Pro Ala Ala Ala Gln Ala Ala Glu Asn Leu Lys Asn Asp Lys Val
225   230   235   240

Ala Ile Val Gly Phe Ser Thr Pro Asn Val Met Arg Pro Tyr Val Glu
         245   250   255

Arg Gly Thr Val Lys Glu Phe Gly Leu Trp Asp Val Val Gln Gln Gly
         260   265   270

Lys Ile Ser Val Tyr Val Ala Asp Ala Leu Leu Lys Lys Gly Ser Met
     275   280   285

Lys Thr Gly Asp Lys Leu Asp Ile Lys Gly Val Gly Gln Val Glu Val

```
              290                    295                      300
Ser Pro Asn Ser Val Gln Gly Tyr Asp Tyr Glu Ala Asp Gly Asn Gly
305                    310                      315                  320
Ile Val Leu Leu Pro Glu Arg Val Ile Phe Asn Lys Glu Asn Ile Gly
                      325                      330                  335
Lys Tyr Asp Phe
              340
```

```
<210> 3...
<211> ...
<212> PRT
<213> E. Coli

<400> 3...

Met Ala Asp Leu Asp Asp Ile Lys Asp Gly Lys Asp Phe Arg Thr Asp
 1                    5                      10                    15
Gln Pro Gln Lys Asn Ile Pro Phe Thr Leu Lys Gly Cys Gly Ala Leu
                      ..                 25                    30
Asp Trp Gly Met Gln Ser Arg Leu Ser Arg Ile Phe Asn Pro Lys Thr
              35                    40                    45
Gly Lys Thr Val Met Leu Ala Phe Asp His Gly Tyr Phe Gln Gly Pro
        50                    55                    60
Thr Thr Gly Leu Glu Arg Ile Asp Ile Asn Ile Ala Pro Leu Phe Glu
65                    70                    75                    80
His Ala Asp Val Leu Met Cys Thr Arg Gly Ile Leu Arg Ser Val Val
                    85                    90                    95
Pro Pro Ala Thr Asn Arg Pro Val Val Leu Arg Ala Ser Gly Ala Asn
              100                   105                   110
Ser Ile Leu Ala Glu Leu Ser Asn Glu Ala Val Ala Leu Ser Met Asp
              115                   120                   125
Asp Ala Val Arg Leu Asn Ser Cys Ala Val Ala Ala Gln Val Tyr Ile
              130                   135                   140
Gly Ser Glu Tyr Glu His Gln Ser Ile Lys Asn Ile Ile Gln Leu Val
              145                   150                   155                   160
Asp Ala Gly Met Lys Val Gly Met Pro Thr Met Ala Val Thr Gly Val
                      165                   170                   175
Gly Lys Asp Met Val Arg Asp Gln Arg Tyr Phe Ser Leu Ala Thr Arg
                      180                   185                   190
Ile Ala Ala Glu Met Gly Ala Gln Ile Ile Lys Thr Tyr Tyr Val Glu
              195                   200                   205
Lys Gly Phe Glu Arg Ile Val Ala Gly Cys Pro Val Pro Ile Val Ile
210                   215                   220
Ala Gly Gly Lys Lys Leu Pro Glu Arg Glu Ala Leu Glu Met Cys Trp
225                   230                   235                   240
Gln Ala Ile Asp Gln Gly Ala Ser Gly Val Asp Met Gly Arg Asn Ile
                      245                   250                   255
Phe Gln Ser Asp His Pro Val Ala Met Met Lys Ala Val Gln Ala Val
                      260                   265                   270
Val His His Asn Glu Thr Ala Asp Arg Ala Tyr Glu Leu Tyr Leu Ser
              275                   280                   285
Glu Lys Gln
              290
```

```
<210> 4
<211> 90
```

<210> PRT
<211> E. Coli

<300> 264

```
Met His Val Thr Leu Val Glu Ile Asn Val His Glu Asp Lys Val Asp
 1               5                   10                  15
Glu Phe Ile Glu Val Phe Arg Gln Asn His Leu Gly Ser Val Gln Glu
                                25                  40
Glu Gly Asn Leu Arg Phe Asp Val Leu Gln Asp Pro Glu Val Asn Ser
            30                  40                  45
Arg Phe Tyr Ile Tyr Glu Ala Tyr Lys Asp Glu Asp Ala Val Ala Phe
        50                  55                  60
His Lys Thr Thr Pro His Tyr Lys Thr Cys Val Ala Lys Leu Glu Ser
65                  70                  75                  80
Leu Met Thr Gly Pro Arg Lys Lys Arg Leu Phe Asn Gly Leu Met Pro
                85                  90                  95
```

<210> 365
<211> 393
<211> PRT
<211> E. Coli

<300> 175

```
Met Phe Gly Pro Met Glu Leu Thr Asn Asp Ala Val Ile Lys Val Ile
 1               5                   10                  15
Gly Val Gly Gly Gly Gly Gly Asn Ala Val Glu His Met Val Arg Glu
                21                  25                  31
Arg Ile Glu Gly Val Glu Phe Phe Ala Val Asn Thr Asp Ala Gln Ala
            35                  40                  45
Leu Arg Lys Thr Ala Val Gly Gln Thr Ile Gln Ile Gly Ser Gly Ile
        50                  55                  60
Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu Val Gly Arg Asn Ala
65                  70                  75                  80
Ala Asp Glu Arg Arg Asp Ala Leu Arg Ala Ala Leu Glu Gly Ala Asp
                90                  90                  95
Met Val Phe Ile Ala Ala Gly Met Gly Gly Gly Thr Gly Thr Gly Ala
                100                 105                 110
Ala Pro Val Val Ala Glu Val Ala Lys Asp Leu Gly Ile Leu Thr Val
        115                 120                 125
Ala Val Val Thr Lys Pro Phe Asn Phe Glu Gly Lys Lys Arg Met Ala
    130                 135                 140
Phe Ala Glu Gln Gly Ile Thr Glu Leu Ser Lys His Val Asp Ser Leu
145                 151                 155                 160
Ile Thr Ile Pro Asn Asp Lys Leu Leu Lys Val Leu Gly Arg Gly Ile
                165                 170                 175
Ser Leu Leu Arg Ala Phe Gly Ala Ala Asn Asp Val Leu Lys Gly Ala
            180                 185                 190
Val Gln Gly Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Met Asn Val
        195                 200                 205
Asp Phe Ala Asp Val Arg Thr Val Met Ser Glu Met Gly Tyr Ala Met
        211                 215                 220
Met Gly Ser Gly Val Ala Ser Gly Glu Asp Arg Ala Glu Glu Ala Ala
225                 230                 235                 240
Glu Met Ala Ile Ser Ser Pro Leu Leu Glu Asp Ile Asp Leu Ser Gly
                245                 250                 255
Ala Arg Gly Val Leu Val Asn Ile Thr Ala Gly Phe Asp Leu Arg Leu
```

```
                260                 265                 270
Asp Glu Phe Glu Thr Val Gly Asn Thr Ile Arg Ala Phe Ala Ser Asp
           275                 280                 285
Asn Ala Thr Val Val Ile Gly Thr Ser Leu Asp Pro Asp Met Asn Asp
      290                 295                 300
Glu Leu Arg Val Thr Val Val Ala Thr Gly Ile Gly Met Asp Lys Arg
305                 310                 315                 320
Pro Glu Ile Thr Leu Val Thr Asn Lys Gln Val Gln Gln Pro Val Met
                325                 330                 335
Asp Arg Tyr Gln Gln His Gly Met Ala Pro Leu Thr Gln Glu Gln Lys
           340                 345                 350
Pro Val Ala Lys Val Val Asn Asp Asn Ala Pro Gln Thr Ala Lys Glu
      355                 360                 365
Pro Asp Tyr Leu Asp Ile Pro Ala Phe Leu Arg Lys Gln Ala Asp
370                 375                 380
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     <210> 266
     <211> 1114
     <212> PRT
     <213> E. Coli

     <400> 266
Met Asp Val Ser Arg Arg Gln Phe Phe Lys Ile Cys Ala Gly Gly Met
1                   5                   10                  15
Ala Gly Thr Thr Val Ala Ala Leu Gly Phe Ala Pro Lys Gln Ala Leu
               20                  25                  30
Ala Gln Ala Arg Asn Tyr Lys Leu Leu Arg Ala Lys Glu Ile Arg Asn
          35                  40                  45
Thr Cys Thr Tyr Cys Ser Val Gly Lys Gly Leu Leu Met Tyr Ser Leu
     50                  55                  60
Gly Asp Gly Ala Lys Asn Ala Arg Glu Ala Ile Tyr His Ile Glu Gly
65                  70                  75                  80
Asp Pro Asp His Pro Val Ser Arg Gly Ala Leu Cys Pro Lys Gly Ala
               85                  90                  95
Gly Leu Leu Asp Tyr Val Asn Ser Glu Asn Arg Leu Arg Tyr Pro Glu
          100                 105                 110
Tyr Arg Ala Pro Gly Ser Asp Lys Trp Gln Arg Ile Ser Trp Glu Glu
          115                 120                 125
Ala Phe Ser Arg Ile Ala Lys Leu Met Lys Ala Asp Arg Asp Ala Asn
     130                 135                 140
Phe Ile Glu Lys Asn Glu Gln Gly Val Thr Val Asn Arg Trp Leu Ser
145                 150                 155                 160
Thr Gly Met Leu Cys Ala Ser Gly Ala Ser Asn Glu Thr Gly Met Leu
               165                 170                 175
Thr Gln Lys Phe Ala Arg Ser Leu Gly Met Leu Ala Val Asp Asn Gln
          180                 185                 190
Ala Arg Val His Gly Pro Thr Val Ala Ser Leu Ala Pro Thr Phe Gly
          195                 200                 205
Arg Gly Ala Met Thr Asn His Trp Val Asp Ile Lys Asn Ala Asn Val
     210                 215                 220
Val Met Val Met Gly Gly Asn Ala Ala Glu Ala His Pro Val Gly Phe
225                 230                 235                 240
Arg Trp Ala Met Glu Ala Lys Asn Asn Asn Asp Ala Thr Leu Ile Val
               245                 250                 255
Val Asp Pro Arg Phe Thr Arg Thr Ala Ser Val Ala Asp Ile Tyr Ala
260                 265                 270
```

```
Pro Ile Arg Ser Gly Thr Asp Ile Thr Phe Leu Ser Gly Val Leu Arg
        275                 280                 285

Tyr Leu Ile Glu Asn Asn Lys Ile Asn Ala Glu Tyr Val Lys His Tyr
    290                 295                 300

Thr Asn Ala Ser Leu Leu Val Arg Asp Asp Phe Ala Phe Glu Asp Gly
305                 310                 315                 320

Leu Phe Ser Gly Tyr Asp Ala Glu Lys Arg Gln Tyr Asp Lys Ser Ser
            325                 330                 335

Trp Asn Tyr Gln Leu Asp Glu Asn Gly Tyr Ala Lys Arg Asp Glu Thr
            340                 345                 350

Leu Thr His Pro Arg Cys Val Trp Asn Leu Leu Lys Glu His Val Ser
        355                 360                 365

Arg Tyr Thr Pro Asp Val Val Glu Asn Ile Cys Gly Thr Pro Lys Ala
    370                 375                 380

Asp Phe Leu Lys Val Cys Glu Val Leu Ala Ser Thr Ser Ala Pro Asp
385                 390                 395                 400

Arg Thr Thr Thr Phe Leu Tyr Ala Leu Gly Trp Thr Gln His Thr Val
            405                 410                 415

Gly Ala Gln Asn Ile Arg Thr Met Ala Met Ile Gln Leu Leu Leu Gly
            420                 425                 430

Asn Met Gly Met Ala Gly Gly Gly Val Asn Ala Leu Arg Gly His Ser
        435                 440                 445

Asn Ile Gln Gly Leu Thr Asp Leu Gly Leu Leu Ser Thr Ser Leu Pro
    450                 455                 460

Gly Tyr Leu Thr Leu Pro Ser Glu Lys Gln Val Asp Leu Gln Ser Tyr
465                 470                 475                 480

Leu Glu Ala Asn Thr Pro Lys Ala Thr Leu Ala Asp Gln Val Asn Tyr
            485                 490                 495

Trp Ser Asn Tyr Pro Lys Phe Phe Val Ser Leu Met Lys Ser Phe Tyr
            500                 505                 510

Gly Asp Ala Ala Gln Lys Glu Asn Asn Trp Gly Tyr Asp Trp Leu Pro
        515                 520                 525

Lys Trp Asp Gln Thr Tyr Asp Val Ile Lys Tyr Phe Asn Met Met Asp
        530                 535                 540

Glu Gly Lys Val Thr Gly Tyr Phe Cys Gln Gly Phe Asn Pro Val Ala
545                 550                 555                 560

Ser Phe Pro Asp Lys Asn Lys Val Val Ser Cys Leu Ser Lys Leu Lys
            565                 570                 575

Tyr Met Val Val Ile Asp Pro Leu Val Thr Glu Thr Ser Thr Phe Trp
        580                 585                 590

Gln Asn His Gly Glu Ser Asn Asp Val Asp Pro Ala Ser Ile Gln Thr
        595                 600                 605

Glu Val Phe Arg Leu Pro Ser Thr Cys Phe Ala Glu Glu Asp Gly Ser
    610                 615                 620

Ile Ala Asn Ser Gly Arg Trp Leu Gln Trp His Trp Lys Gly Gln Asp
615                 640                 645

Ala Pro Gly Glu Ala Arg Asn Asp Gly Glu Ile Leu Ala Gly Ile Tyr
            645                 650                 655

His His Leu Arg Glu Leu Tyr Gln Ser Glu Gly Gly Lys Gly Val Glu
        660                 665                 670

Pro Leu Met Lys Met Ser Trp Asn Tyr Lys Gln Pro His Glu Pro Gln
        675                 680                 685

Ser Asp Glu Val Ala Lys Glu Asn Asn Gly Tyr Ala Leu Glu Asp Leu
    690                 695                 700

Tyr Asp Ala Asn Gly Val Leu Ile Ala Lys Lys Gly Gln Leu Leu Ser
705                 710                 715                 720

Ser Phe Ala His Leu Arg Asp Asp Gly Thr Thr Ala Ser Ser Cys Trp
```

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                    725   730   735
Ile Tyr Thr Gly Ser Trp Thr Glu Gln Gly Asn Gln Met Ala Asn Arg
                740   745   750
Asp Asn Ser Asp Pro Ser Gly Leu Gly Asn Thr Leu Gly Trp Ala Trp
            755   760   765
Ala Trp Pro Leu Asn Arg Arg Val Leu Tyr Asn Arg Ala Ser Ala Asp
        770   775   780
Ile Asn Gly Lys Pro Trp Asp Pro Lys Arg Met Leu Ile Gln Trp Asn
    785   790   795   800
Gly Ser Lys Trp Thr Gly Asn Asp Ile Pro Asp Phe Gly Asn Ala Ala
                805   810   815
Pro Gly Thr Pro Thr Gly Pro Phe Ile Met Gln Pro Glu Gly Met Gly
                820   825   830
Arg Leu Phe Ala Ile Asn Lys Met Ala Glu Gly Pro Phe Pro Glu His
            835   840   845
Tyr Glu Pro Ile Glu Thr Pro Leu Gly Thr Asn Pro Leu His Pro Asn
        850   855   860
Val Val Ser Asn Pro Val Val Arg Leu Tyr Glu Gln Asp Ala Leu Arg
    865   870   875   880
Met Gly Lys Lys Glu Gln Phe Pro Tyr Val Gly Thr Thr Tyr Arg Leu
                885   890   895
Thr Glu His Phe His Thr Trp Thr Lys His Ala Leu Leu Asn Ala Ile
                900   905   910
Ala Gln Pro Glu Gln Phe Val Glu Ile Ser Glu Thr Leu Ala Ala Ala
            915   920   925
Lys Gly Ile Asn Asn Gly Asp Arg Val Thr Val Ser Ser Lys Arg Gly
        930   935   940
Phe Ile Arg Ala Val Ala Val Val Thr Arg Arg Leu Lys Pro Leu Asn
    945   950   955   960
Val Asn Gly Gln Gln Val Glu Thr Val Gly Ile Pro Ile His Trp Gly
                965   970   975
Phe Glu Gly Val Ala Arg Lys Gly Tyr Ile Ala Asn Thr Leu Thr Pro
                980   985   990
Asn Val Gly Arg Ala Asn Ser Gln Thr Pro Glu Tyr Lys Ala Phe Leu
            995   1000   1005
Val Asn Ile Glu Lys Ala
    1010

    <211> 1067
    <211> 244
    <212> PRT
    <213> E. Coli

    <400> 1067
Met Ala Met Glu Thr Gln Asp Ile Ile Lys Arg Ser Ala Thr Asn Ser
 1   5   10   15
Ile Thr Pro Pro Ser Gln Val Arg Asp Tyr Lys Ala Glu Val Ala Lys
                20   25   30
Leu Ile Asp Val Ser Thr Cys Ile Gly Cys Lys Ala Cys Gln Val Ala
            35   40   45
Cys Ser Glu Trp Asn Asp Ile Arg Asp Glu Val Gly His Cys Val Gly
        50   55   60
Val Tyr Asp Asn Pro Ala Asp Leu Ser Ala Lys Ser Trp Thr Val Met
    60   70   75   80
Arg Phe Ser Glu Thr Glu Gln Asn Gly Lys Leu Glu Trp Leu Ile Arg
                85   90   95
Lys Asp Gly Cys Met His Cys Glu Asp Pro Gly Cys Leu Lys Ala Cys

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```
                    100                 105                 110
Pro Ser Ala Gly Ala Ile Ile Gln Tyr Ala Asn Gly Ile Val Asp Phe
    115                 120                 125
Gln Ser Glu Asn Cys Ile Gly Cys Gly Tyr Cys Ile Ala Gly Cys Pro
    130                 135                 140
Phe Asn Ile Pro Arg Leu Asn Lys Glu Asp Asn Arg Val Tyr Lys Cys
145                 150                 155                 160
Thr Leu Cys Val Asp Arg Val Ser Val Gly Gln Glu Pro Ala Cys Val
                    165                 170                 175
Lys Thr Cys Pro Thr Gly Ala Ile His Phe Gly Thr Lys Lys Glu Met
                    180                 185                 190
Leu Glu Leu Ala Glu Gln Arg Val Ala Lys Leu Lys Ala Arg Gly Tyr
                    195                 200                 205
Glu His Ala Gly Val Tyr Asn Pro Glu Gly Val Gly Gly Thr His Val
                    210                 215                 220
Met Tyr Val Leu His His Ala Asp Gln Pro Glu Leu Tyr His Gly Leu
                    225                 230                 235                 240
Pro Lys Asp Pro Lys Ile Asp Thr Ser Val Ser Leu Trp Lys Gly Ala
                    245                 250                 255
Leu Lys Pro Leu Ala Ala Ala Gly Phe Ile Ala Thr Phe Ala Gly Leu
                    260                 265                 270
Ile Phe His Tyr Ile Gly Ile Gly Pro Asn Lys Glu Val Asp Asp Asp
                    275                 280                 285
Glu Glu Asp His His Glu
                    290


    <210> 16
    <211> 217
    <212> PRT
    <213> E. Coli


    <400> 16
Met Ser Lys Ser Lys Met Ile Val Arg Thr Lys Phe Ile Asp Arg Ala
1                   5                   10                  15
Cys His Trp Thr Val Val Ile Cys Phe Phe Leu Val Ala Leu Ser Gly
                    20                  25                  30
Ile Ser Phe Phe Phe Pro Thr Leu Gln Trp Leu Thr Gln Thr Phe Gly
                    35                  40                  45
Thr Pro Gln Met Gly Arg Ile Leu His Pro Phe Phe Gly Ile Ala Ile
50                  55                  60
Phe Val Ala Leu Met Phe Met Phe Val Arg Phe Val His His Asn Ile
65                  70                  75                  80
Pro Asp Lys Lys Arg Ile Pro Trp Leu Leu Asn Ile Val Glu Val Leu
                    85                  90                  95
Lys Gly Asn Glu His Lys Val Ala Asp Val Gly Lys Tyr Asn Ala Gly
                    100                 105                 110
Gln Lys Met Met Phe Trp Ser Ile Met Ser Met Ile Phe Val Leu Leu
                    115                 120                 125
Val Thr Gly Val Ile Ile Trp Arg Pro Tyr Phe Ala Gln Tyr Phe Pro
                    130                 135                 140
Met Gln Val Val Arg Tyr Ser Leu Leu Ile His Ala Ala Ala Gly Ile
145                 150                 155                 160
Ile Leu Ile His Ala Ile Leu Ile His Met Tyr Met Ala Phe Trp Val
                    165                 170                 175
Lys Gly Ser Ile Lys Gly Met Ile Glu Gly Lys Val Ser Arg Arg Trp
                    180                 185                 190
```

Ala Lys Lys His His Pro Arg Trp Tyr Arg Glu Ile Glu Lys Ala Glu
  195   200   205

Ala Lys Lys Glu Ser Glu Glu Gly Ile
  210   215

   (210) 269
   (211) 86
   (212) PRT
   (213) E. Coli

   (400) 269
Met Ala Leu Leu Ile Thr Lys Lys Cys Ile Asn Cys Asp Met Cys Glu
1   5   10   15

Pro Glu Cys Pro Asn Glu Ala Ile Ser Met Gly Asp His Ile Tyr Glu
     20   25   30

Ile Asn Ser Asp Lys Cys Thr Glu Cys Val Gly His Tyr Glu Thr Pro
     35   40   45

Thr Cys Gln Lys Val Cys Pro Ile Pro Asn Thr Ile Val Lys Asp Pro
   50   55   60

Ala His Val Glu Thr Glu Glu Gln Leu Trp Asp Lys Phe Val Leu Met
65   70   75   80

His His Ala Asp Lys Ile
     85

   (210) 270
   (211) 400
   (212) PRT
   (213) E. Coli

   (400) 270
Met Gln Ser Val Asp Val Ala Ile Val Gly Gly Gly Met Val Gly Leu
1   5   10   15

Ala Val Ala Cys Gly Leu Gln Gly Ser Gly Leu Arg Val Ala Val Leu
     20   25   30

Glu Gln Arg Val Gln Glu Pro Leu Ala Ala Asn Ala Pro Pro Gln Leu
     35   40   45

Arg Val Ser Ala Ile Asn Ala Ala Ser Glu Lys Leu Leu Thr Arg Leu
   50   55   60

Gly Val Trp Gln Asp Ile Leu Ser Arg Arg Ala Ser Cys Tyr His Gly
65   70   75   80

Met Glu Val Trp Asp Lys Asp Ser Phe Gly His Ile Ser Phe Asp Asp
     85   90   95

Gln Ser Met Gly Tyr Ser His Leu Gly His Ile Val Glu Asn Ser Val
     100   105   110

Ile His Tyr Ala Leu Trp Asn Lys Ala His Gln Ser Ser Asp Ile Thr
     115   120   125

Leu Leu Ala Pro Ala Glu Leu Gln Gln Val Ala Trp Gly Glu Asn Glu
   130   135   140

Thr Phe Leu Thr Leu Lys Asp Gly Ser Met Leu Thr Ala Arg Leu Val
145   150   155   160

Ile Gly Ala Asp Gly Ala Asn Ser Trp Leu Arg Asn Lys Ala Asp Ile
     165   170   175

Pro Leu Thr Phe Trp Asp Tyr Gln His His Ala Leu Val Ala Thr Ile
     180   185   190

Arg Thr Glu Glu Pro His Asp Ala Val Ala Arg Gln Val Phe His Gly

```
                195                      200                      205
Glu Gly Ile Leu Ala Phe Leu Pro Leu Ser Asp Pro His Leu Cys Ser
     210                      215                      220
Ile Val Trp Ser Leu Ser Pro Glu Glu Ala Gln Arg Met Gln Gln Ala
225                      230                      235                      240
Ser Glu Asp Glu Phe Asn Arg Ala Leu Asn Ile Ala Phe Asp Asn Arg
                    245                      250                      255
Leu Gly Leu Cys Lys Val Glu Ser Ala Arg Gln Val Phe Pro Leu Thr
              260                      265                      270
Gly Arg Tyr Ala Arg Gln Phe Ala Ser His Arg Leu Ala Leu Val Gly
         275                      280                      285
Asp Ala Ala His Thr Ile His Pro Leu Ala Gly Gln Gly Val Asn Leu
         290                      295                      300
Gly Phe Met Asp Ala Ala Glu Leu Ile Ala Glu Leu Lys Arg Leu His
305                      310                      315                      320
Arg Gln Gly Lys Asp Ile Gly Gln Tyr Ile Tyr Leu Arg Arg Tyr Glu
                    325                      330                      335
Arg Ser Arg Lys His Ser Ala Ala Leu Met Leu Ala Gly Met Gln Gly
              340                      345                      350
Phe Arg Asp Leu Phe Ser Gly Thr Asn Pro Ala Lys Lys Leu Leu Arg
         355                      360                      365
Asp Ile Gly Leu Lys Leu Ala Asp Thr Leu Pro Gly Val Lys Pro Gln
         371                      374                      380
Leu Ile Arg Gln Ala Met Gly Leu Asn Asp Leu Pro Glu Trp Leu Arg
385                      390                      395                      400
```

<211> 271
<211> 532
<212> PRT
<213> E. Coli

<400> 271

```
Met Ser Val Ile Ile Val Gly Gly Gly Met Ala Gly Ala Thr Leu Ala
  1                       5                      10                      15
Leu Ala Ile Ser Arg Leu Ser His Gly Ala Leu Pro Val His Leu Ile
                    20                      25                      30
Glu Ala Thr Ala Pro Glu Ser His Ala His Pro Gly Phe Asp Gly Arg
              35                      40                      45
Ala Ile Ala Leu Ala Ala Gly Thr Cys Gln Gln Leu Ala Arg Ile Gly
     50                      55                      60
Val Trp Gln Ser Leu Ala Asp Cys Ala Thr Ala Ile Thr Thr Val His
65                      70                      75                      80
Val Ser Asp Arg Gly His Ala Gly Phe Val Thr Leu Ala Ala Glu Asp
                    85                      90                      95
Tyr Gln Leu Ala Ala Leu Gly Gln Val Val Glu Leu His Asn Val Gly
              100                     105                     110
Gln Arg Leu Phe Ala Leu Leu Arg Lys Ala Pro Gly Val Thr Leu His
         115                     120                     125
Cys Pro Asp Arg Val Ala Asn Val Ala Arg Thr Gln Ser His Val Glu
         130                     135                     140
Val Thr Leu Glu Ser Gly Glu Thr Leu Thr Gly Arg Val Leu Val Ala
145                     150                     155                     160
Ala Asp Gly Thr His Ser Ala Leu Ala Thr Ala Cys Gly Val Asp Trp
                    165                     170                     175
Gln Gln Glu Pro Tyr Glu Gln Leu Ala Val Ile Ala Asn Val Ala Thr
              180                     185                     190
```

Ser Val Ala His Glu Gly Arg Ala Phe Glu Arg Phe Thr Gln His Gly
      185   200   205

Pro Leu Ala Met Leu Pro Met Ser Asp Gly Arg Cys Ser Leu Val Trp
      210   215   220

Cys His Pro Leu Glu Arg Arg Glu Glu Val Leu Ser Trp Ser Asp Glu
  225   230   235   240

Lys Phe Cys Arg Glu Leu Gln Ser Ala Phe Gly Trp Arg Leu Gly Lys
                  245   250   255

Ile Thr His Ala Gly Lys Arg Ser Ala Tyr Pro Leu Ala Leu Thr His
              260   265   270

Ala Ala Arg Ser Ile Thr His Arg Thr Val Leu Val Gly Asn Ala Ala
          275   280   285

Gln Thr Leu His Pro Ile Ala Gly Gln Gly Phe Asn Leu Gly Met Arg
      290   295   300

Asp Val Met Ser Leu Ala Glu Thr Leu Thr Gln Ala Gln Glu Arg Gly
  305   310   315   320

Glu Asp Met Gly Asp Tyr Gly Val Leu Cys Arg Tyr Gln Gln Arg Arg
              325   330   335

Gln Ser Arg Arg Glu Ala Thr Ile Gly Val Thr Asp Ser Leu Val His
          340   345   350

Leu Phe Ala Asn Arg Trp Ala Pro Leu Val Val Gly Arg Asn Ile Gly
          355   360   365

Leu Met Thr Met Glu Leu Phe Thr Pro Ala Arg Asp Val Leu Ala Gln
  370   375   380

Arg Thr Leu Gly Trp Val Ala Arg
  385   390

<210> 17
<211> 443
<212> PRT
<213> E. Coli

<400> 17
Met Ser Glu Ile Ser Arg Gln Glu Phe Gln Arg Arg Arg Gln Ala Leu
  1   5   10   15

Val Glu Gln Met Gln Pro Gly Ser Ala Ala Leu Ile Phe Ala Ala Pro
              20   25   30

Glu Val Thr Arg Ser Ala Asp Ser Glu Tyr Pro Tyr Arg Gln Asn Ser
          35   40   45

Asp Phe Trp Tyr Phe Thr Gly Phe Asn Glu Pro Glu Ala Val Leu Val
      50   55   60

Leu Ile Lys Ser Asp Asp Thr His Asn His Ser Val Leu Phe Asn Arg
  65   70   75   80

Val Arg Asp Leu Thr Ala Glu Ile Trp Phe Gly Arg Arg Leu Gly Gln
              85   90   95

Asp Ala Ala Pro Glu Lys Leu Gly Val Asp Arg Ala Leu Ala Phe Ser
              100   105   110

Glu Ile Asn Gln Gln Leu Tyr Gln Leu Leu Asn Gly Leu Asp Val Val
          115   120   125

Tyr His Ala Gln Gly Glu Tyr Ala Tyr Ala Asp Val Ile Val Asn Ser
      130   135   140

Ala Leu Gln Lys Leu Arg Lys Gly Ser Arg Gln Asn Leu Thr Ala Pro
  145   150   155   160

Ala Thr Met Ile Asp Trp Arg Pro Val Val His Glu Met Arg Leu Phe
              165   170   175

Lys Ser Pro Glu Glu Ile Ala Val Leu Arg Arg Ala Gly Glu Ile Thr

                        180   185   190
Ala Met Ala His Thr Arg Ala Met Glu Lys Cys Arg Pro Gly Met Phe
        195   200   205
Glu Tyr His Leu Glu Gly Glu Ile His His Glu Phe Asn Arg His Gly
    210   215   220
Ala Arg Tyr Pro Ser Tyr Asn Thr Ile Val Gly Ser Gly Glu Asn Gly
225   230   235   240
Cys Ile Leu His Tyr Thr Glu Asn Glu Cys Glu Met Arg Asp Gly Asp
                    245   250   255
Leu Val Leu Ile Asp Ala Gly Cys Glu Tyr Lys Gly Tyr Ala Gly Asp
                    260   265   270
Ile Thr Arg Thr Phe Pro Val Asn Gly Lys Phe Thr Gln Ala Gln Arg
            275   280   285
Glu Ile Tyr Asp Ile Val Leu Glu Ser Leu Glu Thr Ser Leu Arg Leu
        290   295   300
Tyr Arg Pro Gly Thr Ser Ile Leu Glu Val Thr Gly Glu Val Val Arg
305   310   315   320
Ile Met Val Ser Gly Leu Val Lys Leu Gly Ile Leu Lys Gly Asp Val
                    325   330   335
Asp Glu Leu Ile Ala Gln Asn Ala His Arg Pro Phe Phe Met His Gly
            340   345   350
Leu Ser His Trp Leu Gly Leu Asp Val His Asp Val Gly Val Tyr Gly
        355   360   365
Gln Asp Arg Ser Arg Ile Leu Glu Pro Gly Met Val Leu Thr Val Glu
    370   375   380
Pro Gly Leu Tyr Ile Ala Pro Asp Ala Glu Val Pro Glu Gln Tyr Arg
355   390   395   400
Gly Ile Gly Ile Arg Ile Glu Asp Asp Ile Val Ile Thr Glu Thr Gly
                    405   410   415
Asn Glu Asn Leu Thr Ala Ser Val Val Lys Lys Pro Glu Glu Ile Glu
            420   425   430
Ala Leu Met Val Ala Ala Arg Lys Gln
        435   440

    <210> 172
    <211> 194
    <212> PRT
    <213> E. Coli

    <400> 172
Met Leu Met Ser Ile Gln Asn Glu Met Pro Gly Tyr Asn Glu Met Asn
1   5   10   15
Gln Tyr Leu Asn Gln Gln Gly Thr Gly Leu Thr Pro Ala Glu Met His
            20   25   30
Gly Leu Ile Ser Gly Met Ile Lys Gly Gly Asn Asp Asp Ser Ser Trp
        35   40   45
Leu Pro Leu Leu His Asp Leu Thr Asn Glu Gly Met Ala Phe Gly His
        50   55   60
Glu Leu Ala Gln Ala Leu Arg Lys Met His Ser Ala Thr Ser Asp Ala
61   70   75   80
Leu Gln Asp Asp Gly Phe Leu Phe Gln Leu Tyr Leu Pro Asp Gly Asp
                    85   90   95
Asp Val Ser Val Phe Asp Arg Ala Asp Ala Leu Ala Gly Trp Val Asn
                    100   105   110
His Phe Leu Leu Gly Leu Gly Val Thr Gln Pro Lys Leu Asp Lys Val
    115   120   125

Thr Gly Glu Thr Gly Glu Ala Ile Asp Asp Leu Arg Asn Ile Ala Gln
   130   135   140

Leu Gly Tyr Asp Glu Asp Glu Asp Gln Glu Glu Leu Glu Met Ser Leu
   145   150   155   160

Glu Glu Ile Ile Glu Tyr Val Arg Val Ala Ala Leu Leu Cys His Asp
               165   170   175

Thr Phe Thr His Pro Gln Pro Thr Ala Pro Glu Val Gln Lys Pro Thr
           180   185   190

Leu His

<210> 74
<211> 130
<212> PRT
<213> E. Coli

<400> 74
Met Leu Lys Leu Phe Ala Lys Tyr Thr Ser Ile Gly Val Leu Asn Thr
1   5   10   15

Leu Ile His Trp Val Val Phe Gly Val Cys Ile Tyr Val Ala His Thr
             20   25   30

Asn Gln Ala Leu Ala Asn Phe Ala Gly Phe Val Val Ala Val Ser Phe
         35   40   45

Ser Phe Phe Ala Asn Ala Lys Phe Thr Phe Lys Ala Ser Thr Thr Thr
    50   55   60

Met Arg Tyr Met Leu Tyr Val Gly Phe Met Gly Thr Leu Ser Ala Thr
65   70   75   80

Val Gly Trp Ala Ala Asp Arg Cys Ala Leu Pro Pro Met Ile Thr Leu
             85   90   95

Val Thr Phe Ser Ala Ile Ser Leu Val Cys Gly Phe Val Tyr Ser Lys
         100   105   110

Phe Ile Val Phe Arg Asp Ala Lys
         115   120

<210> 75
<211> 126
<212> PRT
<213> E. Coli

<400> 75
Met Lys Ile Ser Leu Val Val Pro Val Phe Asn Glu Glu Glu Ala Ile
1   5   10   15

Pro Ile Phe Tyr Lys Thr Val Arg Glu Phe Glu Glu Leu Lys Ser Tyr
             20   25   30

Glu Val Gln Ile Val Phe Ile Asn Asp Gly Ser Lys Asp Ala Thr Glu
    35   40   45

Ser Ile Ile Asn Ala Leu Ala Val Ser Asp Pro Leu Val Val Pro Leu
    50   55   60

Ser Phe Thr Arg Asn Phe Gly Lys Glu Pro Ala Leu Phe Ala Gly Leu
65   70   75   80

Asp His Ala Thr Gly Asp Ala Ile Ile Pro Ile Asp Val Asp Leu Gln
             85   90   95

Asp Pro Ile Glu Val Ile Pro His Leu Ile Glu Lys Trp Gln Ala Gly
         100   105   110

Ala Asp Met Val Leu Ala Lys Arg Ser Asp Arg Ser Thr Asp Gly Arg
         115   120   125

Leu Lys Arg Lys Thr Ala Glu Trp Phe Tyr Lys Leu His Asn Lys Ile
    130   135   140
Ser Asn Pro Lys Ile Glu Glu Asn Val Gly Asp Phe Arg Leu Met Ser
145   150   155   160
Arg Asp Val Val Glu Asn Ile Lys Leu Met Pro Glu Arg Asn Leu Phe
                165   170   175
Met Lys Gly Ile Leu Ser Trp Val Gly Gly Lys Thr Asp Ile Val Glu
                180   185   190
Tyr Val Arg Ala Glu Arg Ile Ala Gly Asp Thr Lys Phe Asn Gly Trp
                195   200   205
Lys Leu Trp Asn Leu Ala Leu Glu Gly Ile Thr Ser Phe Ser Thr Phe
    210   215   220
Pro Leu Arg Ile Trp Thr Tyr Ile Gly Leu Val Val Ala Ser Val Ala
225   230   235   240
Phe Ile Tyr Gly Ala Trp Met Ile Leu Asp Thr Ile Ile Phe Gly Asn
                245   250   255
Ala Val Arg Gly Tyr Pro Ser Leu Leu Val Ser Ile Leu Phe Leu Gly
                260   265   270
Gly Ile Gln Met Ile Gly Ile Gly Val Leu Gly Glu Tyr Ile Gly Arg
                275   280   285
Thr Tyr Ile Glu Thr Lys Lys Arg Pro Lys Tyr Ile Ile Lys Arg Val
    290   295   300
Lys Lys
305

      <210> 276
      <211> 443
      <212> PRT
      <213> E. Coli

      <400> 276
Met Asn Lys Ala Ile Lys Val Ser Leu Tyr Ile Ser Phe Val Leu Ile
  1   5   10   15
Ile Cys Ala Leu Ser Lys Asn Ile Met Met Leu Asn Thr Ser Asp Phe
                20   25   30
Gly Arg Ala Ile Lys Pro Leu Ile Glu Asp Ile Pro Ala Phe Thr Tyr
                35   40   45
Asp Leu Pro Leu Leu Tyr Lys Leu Lys Gly His Ile Asp Ser Ile Asp
    50   55   60
Ser Tyr Glu Tyr Ile Ser Ser Tyr Ser Tyr Ile Leu Tyr Thr Tyr Val
65   70   75   80
Leu Phe Ile Ser Ile Phe Thr Glu Tyr Leu Asp Ala Arg Val Leu Ser
                85   90   95
Leu Phe Leu Lys Val Ile Tyr Ile Tyr Ser Leu Tyr Ala Ile Phe Thr
                100   105   110
Ser Tyr Ile Lys Thr Glu Arg Tyr Val Thr Leu Phe Thr Phe Phe Ile
                115   120   125
Leu Ala Phe Leu Met Cys Ser Ser Ser Thr Leu Ser Met Phe Ala Ser
                130   135   140
Phe Tyr Gln Glu Gln Ile Val Ile Ile Phe Leu Pro Phe Leu Val Tyr
145   150   155   160
Ser Leu Thr Cys Lys Asn Asn Lys Ser Met Leu Leu Leu Phe Phe Ser
                165   170   175
Leu Leu Ile Ile Ser Thr Ala Lys Asn Gln Phe Ile Leu Thr Pro Leu
                180   185   190
Ile Val Tyr Ser Tyr Tyr Ile Phe Phe Asp Arg His Lys Leu Ile Ile

```
              195                    200                    205
Lys Ser Val Ile Cys Val Val Cys Leu Leu Ala Ser Ile Phe Ala Ile
210                    215                    220
Ser Tyr Ser Lys Gly Val Val Glu Leu Asn Lys Tyr His Ala Thr Tyr
225                    230                    235                    240
Phe Gly Ser Tyr Leu Tyr Met Lys Asn Asn Gly Tyr Lys Met Pro Ser
               245                    250                    255
Tyr Val Asp Asp Lys Cys Val Gly Leu Asp Ala Trp Gly Asn Lys Phe
               260                    265                    270
Asp Ile Ser Phe Gly Ala Thr Pro Thr Glu Val Gly Thr Glu Cys Phe
               275                    280                    285
Glu Ser His Lys Asp Glu Thr Phe Ser Asn Ala Leu Phe Leu Leu Val
     290                    295                    300
Ser Lys Pro Ser Thr Ile Phe Lys Leu Pro Phe Asp Asp Gly Val Met
305                    310                    315                    320
Ser Gln Tyr Lys Glu Asn Tyr Phe His Val Tyr Lys Lys Leu His Val
               325                    330                    335
Ile Tyr Gly Glu Ser Asn Ile Leu Thr Thr Ile Thr Asn Ile Lys Asp
               340                    345                    350
Asn Ile Phe Lys Asn Ile Arg Phe Ile Ser Leu Leu Leu Phe Phe Ile
               355                    360                    365
Ala Ser Ile Phe Ile Arg Asn Asn Lys Ile Lys Ala Ser Leu Phe Val
     370                    375                    380
Val Ser Leu Phe Gly Ile Ser Gln Phe Tyr Val Ser Phe Phe Gly Glu
385                    390                    395                    400
Gly Tyr Arg Asp Leu Ser Lys His Leu Phe Gly Met Tyr Phe Ser Phe
               405                    410                    415
Asp Leu Cys Leu Tyr Ile Thr Val Val Phe Leu Ile Tyr Lys Ile Ile
               420                    425                    430
Gln Arg Asn Gln Asp Asn Ser Asp Val Lys His
               435                    440
```

```
Met Gly Ile Leu Ser Trp Ile Ile Phe Gly Leu Ile Ala Gly Ile Leu
1                     5                    10                    15
Ala Lys Trp Ile Met Pro Gly Lys Asp Gly Gly Gly Phe Phe Met Thr
               20                    25                    30
Ile Leu Leu Gly Ile Val Gly Ala Val Val Gly Gly Trp Ile Ser Thr
               35                    40                    45
Leu Phe Gly Phe Gly Lys Val Asp Gly Phe Asn Phe Gly Ser Phe Val
     50                    55                    60
Val Ala Val Ile Gly Ala Ile Val Val Leu Phe Ile Tyr Arg Lys Ile
65                    70                    75                    80
Lys Ser
```

<213> E. Coli

<400> 278
```
Met Gly Lys Ala Thr Tyr Thr Val Thr Val Thr Asn Asn Ser Asn Gly
1               5                   10                  15
Val Ser Val Asp Tyr Glu Thr Glu Thr Pro Met Thr Leu Leu Val Pro
            20                  25                  30
Glu Val Ala Ala Glu Val Ile Lys Asp Leu Val Asn Thr Val Arg Ser
            35                  40                  45
Tyr Asp Thr Glu Asn Glu His Asp Val Cys Gly Trp
            50                  55                  60
```

<210> 279
<211> 119
<212> PRT
<213> E. Coli

<400> 279
```
Met Leu Gln Ile Pro Gln Asn Tyr Ile His Thr Arg Ser Thr Pro Phe
1               5                   10                  15
Trp Asn Lys Gln Thr Ala Pro Ala Gly Ile Phe Glu Arg His Leu Asp
            20                  25                  30
Lys Gly Thr Arg Pro Gly Val Tyr Pro Arg Leu Ser Val Met His Gly
            35                  40                  45
Ala Val Lys Tyr Leu Gly Tyr Ala Asp Glu His Ser Ala Glu Pro Asp
            51                  55                  60
Gln Val Ile Leu Ile Glu Ala Gly Gln Phe Ala Val Phe Pro Pro Glu
65                  70                  75                  80
Lys Trp His Asn Ile Glu Ala Met Thr Asp Asp Thr Tyr Phe Asn Ile
            85                  90                  95
Asp Phe Phe Val Ala Pro Glu Val Leu Met Glu Gly Ala Gln Gln Arg
            100                 105                 110
Lys Val Ile His Asn Gly Lys
            115
```

<210> 280
<211> 146
<212> PRT
<213> E. Coli

<400> 280
```
Met Lys Phe Lys Val Ile Ala Leu Ala Ala Leu Met Gly Ile Ser Gly
1               5                   10                  15
Met Ala Ala Gln Ala Asn Glu Leu Pro Asp Gly Pro His Ile Val Thr
            20                  25                  30
Ser Gly Thr Ala Ser Val Asp Ala Val Pro Asp Ile Ala Thr Leu Ala
            35                  40                  45
Ile Gly Val Asn Val Ala Ala Lys Asp Ala Ala Thr Ala Lys Lys Gln
            50                  55                  60
Ala Asp Gln Arg Val Ala Gln Tyr Ile Ser Phe Leu Glu Leu Asn Gln
65                  70                  75                  80
Ile Ala Lys Lys Asp Ile Ser Ser Ala Asn Leu Arg Thr Gln Pro Asp
            85                  90                  95
Tyr Asp Tyr Gln Asp Gly Lys Ser Ile Leu Lys Gly Tyr Arg Ala Val
            100                 105                 110
```

Arg Thr Val Glu Val Thr Leu Arg Gln Leu Asp Lys Leu Asn Ser Leu
        115   120   125
Leu Asp Gly Ala Leu Lys Ala Gly Leu Asn Glu Ile Arg Ser Val Ser
        130   135   140
Leu Gly Val Ala Gln Pro Asp Ala Tyr Lys Asp Lys Ala Arg Lys Ala
145   150   155   160
Ala Ile Asp Asn Ala Ile His Gln Ala Gln Glu Leu Ala Asn Gly Phe
                165   170   175
His Arg Lys Leu Gly Pro Val Tyr Ser Val Arg Tyr His Val Ser Asn
            180   185   190
Tyr Gln Pro Ser Pro Met Val Arg Met Met Lys Ala Asp Ala Ala Pro
            195   200   205
Val Ser Ala Gln Glu Thr Tyr Glu Gln Ala Ala Ile Gln Phe Asp Asp
    210   215   220
Gln Val Asp Val Val Phe Gln Leu Glu Pro Val Asp Gln Gln Pro Ala
225   230   235   240
Lys Thr Pro Ala Ala Gln
            245

    <210> 291
    <211> 464
    <212> PRT
    <213> E. Coli

    <400> 291
Met Leu Leu Leu Asp Ala Cys Ser Gln Met Cys Pro Ser Phe Arg Arg
  1   5   10   15
Phe Gln Thr Val Phe His Asn Ser Ser Ile Phe Leu Pro Tyr Trp Leu
            20   25   30
Ala Thr Leu Val Ser Phe Arg Glu Thr Phe Gln Glu Glu Lys Leu Leu
            35   40   45
Thr Met Lys Gly Ser Tyr Lys Ser Arg Trp Val Ile Val Ile Val Val
        50   55   60
Val Ile Ala Ala Ile Ala Ala Phe Trp Phe Trp Gln Gly Arg Asn Asp
65   70   75   80
Ser Arg Ser Ala Ala Pro Gly Ala Thr Lys Gln Ala Gln Gln Ser Pro
                85   90   95
Ala Gly Gly Arg Arg Gly Met Arg Ser Gly Pro Leu Ala Pro Val Gln
            100   105   110
Ala Ala Thr Ala Val Glu Gln Ala Val Pro Arg Tyr Leu Thr Gly Leu
        115   120   125
Gly Thr Ile Thr Ala Ala Asn Thr Val Thr Val Arg Ser Arg Val Asp
        130   135   140
Gly Gln Leu Ile Ala Leu His Phe Gln Glu Gly Gln Gln Val Lys Ala
145   150   155   160
Gly Asp Leu Leu Ala Glu Ile Asp Pro Ser Gln Phe Lys Val Ala Leu
                165   170   175
Ala Gln Ala Gln Gly Gln Leu Ala Lys Asp Lys Ala Thr Leu Ala Asn
            180   185   190
Ala Arg Arg Asp Leu Ala Arg Tyr Gln Gln Leu Ala Lys Thr Asn Leu
        19   200   205
Val Ser Arg Gln Glu Leu Asp Ala Gln Gln Ala Leu Val Ser Glu Thr
    210   215   220
Glu Gly Thr Ile Lys Ala Asp Glu Ala Ser Val Ala Ser Ala Gln Leu
225   230   235   241
Gln Leu Asp Trp Ser Arg Ile Thr Ala Pro Val Asp Gly Arg Val Gly

```
                    245                  250                  255
Leu Lys Gln Val Asp Val Gly Asn Gln Ile Ser Ser Gly Asp Thr Thr
                260                  265                  270
Gly Ile Val Val Ile Thr Gln Thr His Pro Ile Asp Leu Val Phe Thr
                275                  280                  285
Leu Pro Glu Ser Asp Ile Ala Thr Val Val Gln Ala Gln Lys Ala Gly
            290                  295                  300
Lys Pro Leu Val Val Glu Ala Trp Asp Arg Thr Asn Ser Lys Lys Leu
305                  310                  315                  320
Ser Glu Gly Thr Leu Leu Ser Leu Asp Asn Gln Ile Asp Ala Thr Thr
                325                  330                  335
Gly Thr Ile Lys Val Lys Ala Arg Phe Asn Asn Gln Asp Asp Ala Leu
                340                  345                  350
Phe Pro Asn Gln Phe Val Asn Ala Arg Met Leu Val Asp Thr Glu Gln
            355                  360                  365
Asn Ala Val Val Ile Pro Thr Ala Ala Leu Gln Met Gly Asn Glu Gly
            370                  375                  380
His Phe Val Trp Val Leu Asn Ser Glu Asn Lys Val Ser Lys His Leu
385                  390                  395                  400
Val Thr Pro Gly Ile Gln Asp Ser Gln Lys Val Val Ile Arg Ala Gly
                405                  410                  415
Ile Ser Ala Gly Asp Arg Val Val Thr Asp Gly Ile Asp Arg Leu Thr
            420                  425                  430
Glu Gly Ala Tyr Val Glu Val Val Glu Ala Gln Ser Ala Thr Thr Pro
            435                  440                  445
Glu Glu Lys Ala Thr Ser Arg Glu Tyr Ala Lys Lys Gly Ala Arg Ser
    450                  455                  460
```

(210) 161
(211) 1640
(212) PRT
(213) N. Coli

(400) 161

```
Met Gln Val Leu Pro Pro Ser Ser Thr Gly Gly Pro Ser Arg Leu Phe
1                   5                   11                  15
Ile Met Arg Pro Val Ala Thr Thr Leu Leu Met Val Ala Ile Leu Leu
                    21                  25                  30
Ala Gly Ile Ile Gly Tyr Arg Ala Leu Pro Val Ser Ala Leu Pro Glu
            35                  40                  45
Val Asp Tyr Pro Thr Ile Gln Val Val Thr Leu Tyr Pro Gly Ala Ser
        50                  55                  60
Pro Asp Val Met Thr Ser Ala Val Thr Ala Pro Leu Glu Arg Gln Phe
65                  70                  75                  80
Gly Gln Met Ser Gly Leu Lys Gln Met Ser Ser Gln Ser Ser Gly Gly
                85                  90                  95
Ala Ser Val Ile Thr Leu Gln Phe Gln Leu Thr Leu Pro Leu Asp Val
                100                 105                 110
Ala Glu Gln Gln Val Gln Ala Ala Ile Asn Ala Ala Thr Asn Leu Leu
            115                 120                 125
Pro Ser Asp Leu Pro Asn Pro Pro Val Tyr Ser Lys Val Asn Pro Ala
        130                 135                 140
Asp Pro Pro Ile Met Thr Leu Ala Val Thr Ser Thr Ala Met Pro Met
145                 150                 155                 160
Thr Gln Val Glu Asp Met Val Glu Thr Arg Val Ala Gln Lys Ile Ser
                165                 170                 175
```

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Gln Ile Ser Gly Val Gly Leu Val Thr Leu Ser Gly Gly Gln Arg Pro
                    180   185   190

Ala Val Arg Val Lys Leu Asn Ala Gln Ala Ile Ala Ala Leu Gly Leu
          195   200   205

Thr Ser Glu Thr Val Arg Thr Ala Ile Thr Gly Ala Asn Val Asn Ser
          210   215   220

Ala Lys Gly Ser Leu Asp Gly Pro Ser Arg Ala Val Thr Leu Ser Ala
225   230   235   240

Asn Asp Gln Met Gln Ser Ala Glu Glu Tyr Arg Gln Leu Ile Ile Ala
                    245   250   255

Tyr Gln Asn Gly Ala Pro Ile Arg Leu Gly Asp Val Ala Thr Val Glu
                    260   265   270

Gln Gly Ala Glu Asn Ser Trp Leu Gly Ala Trp Ala Asn Lys Glu Gln
                    275   280   285

Ala Ile Val Met Asn Val Gln Arg Gln Pro Gly Ala Asn Ile Ile Ser
          290   295   300

Thr Ala Asp Ser Ile Arg Gln Met Leu Pro Gln Leu Thr Glu Ser Leu
305   310   315   320

Pro Lys Ser Val Lys Val Thr Val Leu Ser Asp Arg Thr Thr Asn Ile
                    325   330   335

Arg Ala Ser Val Asp Asp Thr Gln Phe Glu Leu Met Met Ala Ile Ala
          340   345   350

Leu Val Val Met Ile Ile Tyr Leu Phe Leu Arg Asn Ile Pro Ala Thr
          355   360   365

Ile Ile Pro Gly Val Ala Val Pro Leu Ser Leu Ile Gly Thr Phe Ala
    371   375   380

Val Met Val Phe Leu Asp Phe Ser Ile Asn Asn Leu Thr Leu Met Ala
385   390   395   400

Leu Thr Ile Ala Thr Gly Phe Val Val Asp Asp Ala Ile Val Val Ile
          405   410   415

Glu Asn Ile Ser Arg Tyr Ile Glu Lys Gly Glu Lys Pro Leu Ala Ala
          420   425   430

Ala Leu Lys Gly Ala Gly Glu Ile Gly Phe Thr Ile Ile Ser Leu Thr
          435   440   445

Phe Ser Leu Ile Ala Val Leu Ile Pro Leu Leu Phe Met Gly Asp Ile
    450   455   460

Val Gly Arg Leu Phe Arg Glu Phe Ala Ile Thr Leu Ala Val Ala Ile
465   470   475   480

Leu Ile Ser Ala Val Val Ser Leu Thr Leu Thr Pro Met Met Cys Ala
          485   490   495

Arg Met Leu Ser Gln Glu Ser Leu Arg Lys Gln Asn Arg Phe Ser Arg
              500   505   510

Ala Ser Glu Lys Met Phe Asp Arg Ile Ile Ala Ala Tyr Gly Arg Gly
          515   520   525

Leu Ala Lys Val Leu Asn His Pro Trp Leu Thr Leu Ser Val Ala Leu
    530   535   540

Ser Thr Leu Leu Leu Ser Val Leu Leu Trp Val Phe Ile Pro Lys Gly
545   550   555   560

Phe Pro Pro Val Gln Asp Asn Gly Ile Ile Gln Gly Thr Leu Gln Ala
              565   570   575

Pro Gln Ser Ser Ser Phe Ala Asn Met Ala Gln Arg Gln Arg Gln Val
          580   585   590

Ala Asp Val Ile Leu Gln Asp Pro Ala Val Gln Ser Leu Thr Ser Phe
          595   600   605

Val Gly Val Asp Gly Thr Asn Pro Ser Leu Asn Ser Ala Arg Leu Gln
610   615   620

Ile Asn Leu Lys Pro Leu Asp Glu Arg Asp Asp Arg Val Gln Lys Val

```
625                    630                    635                    640
Ile Ala Arg Leu Gln Thr Ala Val Asp Lys Val Pro Gly Val Asp Leu
                645                    650                    655
Phe Leu Gln Pro Thr Gln Asp Leu Thr Ile Asp Thr Gln Val Ser Arg
                660                    665                    670
Thr Gln Tyr Gln Phe Thr Leu Gln Ala Thr Ser Leu Asp Ala Leu Ser
                675                    680                    685
Thr Trp Val Pro Gln Leu Met Glu Lys Leu Gln Gln Leu Pro Gln Leu
                690                    695                    700
Ser Asp Val Ser Ser Asp Trp Gln Asp Lys Gly Leu Val Ala Tyr Val
705                    710                    715                    720
Asn Val Asp Arg Asp Ser Ala Ser Arg Leu Gly Ile Ser Met Ala Asp
                725                    730                    735
Val Asp Asn Ala Leu Tyr Asn Ala Phe Gly Gln Arg Leu Ile Ser Thr
                740                    745                    750
Ile Tyr Thr Gln Ala Asn Gln Tyr Arg Val Val Leu Glu His Asn Thr
                755                    760                    765
Glu Asn Thr Pro Gly Leu Ala Ala Leu Asp Thr Ile Arg Leu Thr Ser
        770                    775                    780
Ser Asp Gly Gly Val Val Pro Leu Ser Ser Ile Ala Lys Ile Glu Gln
765                    790                    795                    800
Arg Phe Ala Pro Leu Ser Ile Asn His Leu Asp Gln Phe Pro Val Thr
                805                    810                    815
Thr Ile Ser Phe Asn Val Pro Asp Asn Tyr Ser Leu Gly Asp Ala Val
                820                    825                    830
Gln Ala Ile Met Asp Thr Glu Lys Thr Leu Asn Leu Pro Val Asp Ile
                835                    840                    845
Thr Thr Gln Phe Gln Gly Ser Thr Leu Ala Phe Gln Ser Ala Leu Gly
        850                    855                    860
Ser Thr Val Trp Leu Ile Val Ala Ala Val Val Ala Met Tyr Ile Val
865                    870                    875                    880
Leu Gly Ile Leu Tyr Glu Ser Phe Ile His Pro Ile Thr Ile Leu Ser
                885                    890                    895
Thr Leu Pro Thr Ala Gly Val Gly Ala Leu Leu Ala Leu Leu Ile Ala
                900                    905                    910
Gly Ser Glu Leu Asp Val Ile Ala Ile Ile Gly Ile Ile Leu Leu Ile
                915                    920                    925
Gly Ile Val Lys Lys Asn Ala Ile Met Met Ile Asp Phe Ala Leu Ala
        930                    935                    940
Ala Glu Arg Glu Gln Gly Met Ser Pro Arg Glu Ala Ile Tyr Gln Ala
945                    950                    955                    960
Cys Leu Leu Arg Phe Arg Pro Ile Leu Met Thr Thr Leu Ala Ala Leu
                965                    970                    975
Leu Gly Ala Leu Pro Leu Met Leu Ser Thr Gly Val Gly Ala Glu Leu
        980                    985                    990
Arg Arg Pro Leu Gly Ile Gly Met Val Gly Gly Leu Ile Val Ser Gln
995                    1000                   1005
Val Leu Thr Leu Phe Thr Thr Pro Val Ile Tyr Leu Leu Phe Asp Arg
        1010                   1015                   1020
Leu Ala Leu Trp Thr Lys Ser Arg Phe Ala Arg His Glu Glu Glu Ala
1025                   1030                   1035                   1040
```

        <210> 265
        <211> 1025
        <212> PRT
        <213> E. Coli

```
Met Lys Phe Phe Ala Leu Phe Ile Tyr Arg Pro Val Ala Thr Ile Leu
1               5               10              15

Leu Ser Val Ala Ile Thr Leu Cys Gly Ile Leu Gly Phe Arg Met Leu
            20              25              30

Pro Val Ala Pro Leu Pro Gln Val Asp Phe Pro Val Ile Ile Val Ser
            35              40              45

Ala Ser Leu Pro Gly Ala Ser Pro Glu Thr Met Ala Ser Ser Val Ala
            50              55              60

Thr Pro Leu Glu Arg Ser Leu Gly Arg Ile Ala Gly Val Ser Glu Met
65                  70              75              90

Thr Ser Ser Ser Ser Leu Gly Ser Thr Arg Ile Ile Leu Gln Phe Asp
                85              90              95

Phe Asp Arg Asp Ile Asn Gly Ala Ala Arg Asp Val Gln Ala Ala Ile
                100             105             110

Asn Ala Ala Gln Ser Leu Leu Pro Ser Gly Met Pro Ser Arg Pro Thr
            115             120             125

Tyr Arg Lys Ala Asn Pro Ser Asp Ala Pro Ile Met Ile Leu Thr Leu
            130             135             140

Thr Ser Asp Thr Tyr Ser Gln Gly Glu Leu Tyr Asp Phe Ala Ser Thr
145             150             155             160

Gln Leu Ala Pro Thr Ile Ser Gln Ile Asp Gly Val Gly Asp Val Asp
                165             170             175

Val Gly Gly Ser Ser Leu Pro Ala Val Arg Val Gly Leu Asn Pro Gln
                180             185             190

Ala Leu Phe Asn Gln Gly Val Ser Leu Asp Asp Val Arg Thr Ala Val
            195             200             205

Ser Asn Ala Asn Val Arg Lys Pro Gln Gly Ala Leu Glu Asp Gly Thr
            210             215             220

His Arg Trp Gln Ile Gln Thr Asn Asp Glu Leu Lys Thr Ala Ala Glu
225             230             235             240

Tyr Gln Pro Leu Ile Ile His Tyr Asn Asn Gly Gly Ala Val Arg Leu
                245             250             255

Gly Asp Val Ala Thr Val Thr Asp Ser Val Gln Asp Val Arg Asn Ala
                260             265             270

Gly Met Thr Asn Ala Lys Pro Ala Ile Leu Leu Met Ile Arg Lys Leu
            275             280             285

Pro Gln Ala Asn Ile Ile Gln Thr Val Asp Ser Ile Arg Ala Lys Leu
            290             295             300

Pro Gln Leu Gln Glu Thr Ile Pro Ala Ala Ile Asp Leu Gln Ile Ala
305             310             315             320

Gln Asp Arg Ser Pro Thr Ile Arg Ala Ser Leu Glu Glu Val Glu Gln
                325             330             335

Thr Leu Ile Ile Ser Val Ala Leu Val Ile Leu Val Val Phe Leu Phe
                340             345             350

Leu Arg Ser Gly Arg Ala Thr Ile Ile Pro Ala Val Ser Val Pro Val
            355             360             365

Ser Leu Ile Gly Thr Phe Ala Ala Met Tyr Leu Cys Gly Phe Ser Leu
            370             375             380

Asn Asn Leu Ser Leu Met Ala Leu Thr Ile Ala Thr Gly Phe Val Val
385             390             395             400

Asp Asp Ala Ile Val Val Leu Glu Asn Ile Ala Arg His Leu Glu Ala
                405             410             415

Gly Met Lys Pro Leu Gln Ala Ala Leu Gln Gly Thr Arg Glu Val Gly
            420             425             430

Phe Thr Val Leu Ser Met Ser Leu Ser Leu Val Ala Val Phe Leu Pro
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              435               440               445
Leu Leu Leu Met Gly Gly Leu Pro Gly Arg Leu Leu Arg Glu Phe Ala
    450               455               460
Val Thr Leu Ser Val Ala Ile Gly Ile Ser Leu Leu Val Ser Leu Thr
465               470               475               480
Leu Thr Pro Met Met Cys Gly Trp Met Leu Lys Ala Ser Lys Pro Arg
                  485               490               495
Glu Gln Lys Arg Leu Arg Gly Phe Gly Arg Met Leu Val Ala Leu Gln
                  500               505               510
Gln Gly Tyr Gly Lys Ser Leu Lys Trp Val Leu Asn His Thr Arg Leu
                  515               520               525
Val Gly Val Val Leu Leu Gly Thr Ile Ala Leu Asn Ile Trp Leu Tyr
                  530               535               540
Ile Ser Ile Pro Lys Thr Phe Phe Pro Glu Gln Asp Thr Gly Val Leu
545               550               555               560
Met Gly Gly Ile Gln Ala Asp Gln Ser Ile Ser Phe Gln Ala Met Arg
                  565               570               575
Gly Lys Leu Gln Asp Phe Met Lys Ile Ile Arg Asp Asp Pro Ala Val
                  580               585               590
Asp Asn Val Thr Gly Phe Thr Gly Gly Ser Arg Val Asn Ser Gly Met
                  595               600               605
Met Phe Ile Thr Leu Lys Pro Arg Asp Glu Arg Ser Gln Thr Ala Gln
                  610               615               620
Gln Ile Ile Asp Arg Leu Arg Val Lys Leu Ala Lys Glu Pro Gly Ala
625               630               635               640
Asn Leu Phe Leu Met Ala Val Gln Asp Ile Arg Val Gly Gly Arg Gln
                  645               650               655
Ser Asn Ala Ser Tyr Gln Tyr Thr Leu Leu Ser Asp Asp Leu Ala Ala
                  660               665               670
Leu Arg Glu Trp Glu Pro Lys Ile Arg Lys Lys Leu Ala Thr Leu Pro
                  675               680               685
Glu Leu Ala Asp Val Asn Ser Asp Gln Gln Asp Asn Gly Ala Glu Met
                  690               695               700
Asn Leu Val Tyr Asp Arg Asp Thr Met Ala Arg Leu Gly Ile Asp Val
705               710               715               720
Gln Ala Ala Asn Ser Leu Leu Asn Asn Ala Phe Gly Gln Arg Gln Ile
                  725               730               735
Ser Thr Ile Tyr Gln Pro Met Asn Gln Tyr Lys Val Val Met Glu Val
                  740               745               750
Asp Pro Arg Tyr Thr Gln Asp Ile Ser Ala Leu Glu Lys Met Phe Val
                  755               760               765
Ile Asn Asn Glu Gly Lys Ala Ile Pro Leu Ser Tyr Phe Ala Lys Trp
    770               775               780
Gln Pro Ala Asn Ala Pro Leu Ser Val Asn His Gln Gly Leu Ser Ala
785               790               795
Ala Ser Thr Ile Ser Phe Asn Leu Pro Thr Gly Lys Ser Leu Ser Asp
                  800               805               810
Ala Ser Ala Ala Ile Asp Arg Ala Met Thr Gln Leu Gly Val Pro Ser
                  815               820               825
Thr Val Arg Gly Ser Phe Ala Gly Thr Ala Gln Val Phe Gln Glu Thr
                  830               835               840
Met Asn Ser Gln Val Ile Leu Ile Ile Ala Ala Ile Ala Thr Val Tyr
                  845               850               855
Ile Val Leu Gly Ile Leu Tyr Glu Ser Tyr Val His Pro Leu Thr Ile
865               870               875               880
Leu Ser Thr Leu Pro Ser Ala Gly Val Gly Ala Leu Leu Ala Leu Glu
                  885               890               895
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Leu Phe Asn Ala Pro Phe Ser Leu Ile Ala Leu Ile Gly Ile Met Leu
            900   905   910

Leu Ile Gly Ile Val Lys Lys Asn Ala Ile Met Met Val Asp Phe Ala
            915   920   925

Leu Glu Ala Gln Arg His Gly Asn Leu Thr Pro Gln Glu Ala Ile Phe
            930   935   940

Gln Ala Cys Leu Leu Arg Phe Arg Pro Ile Met Met Thr Thr Leu Ala
945   950   955   960

Ala Leu Phe Gly Ala Leu Pro Leu Val Leu Ser Gly Gly Asp Gly Ser
                  965   970   975

Glu Leu Arg Gln Pro Leu Gly Ile Thr Ile Val Gly Gly Leu Val Met
            980   985   990

Ser Gln Leu Leu Thr Leu Tyr Thr Thr Pro Val Val Tyr Leu Phe Phe
            995   1000   1005

Asp Arg Leu Arg Leu Arg Phe Ser Arg Lys Pro Lys Gln Thr Val Thr
            1010   1015   1020

Glu
1025

        <210> 284
        <211> 371
        <212> PRT
        <213> E. Coli

        <400> 284
Met Thr Asp Leu Pro Asp Ser Thr Arg Trp Gln Leu Trp Ile Val Ala
1   5   10   15

Phe Gly Phe Phe Met Gln Ser Leu Asp Thr Thr Ile Val Asn Thr Ala
            20   23   30

Leu Pro Ser Met Ala Gln Ser Leu Gly Glu Ser Pro Leu His Met His
            35   40   45

Met Val Ile Val Ser Tyr Val Leu Thr Val Ala Val Met Leu Pro Ala
            50   55   60

Ser Gly Trp Leu Ala Asp Lys Val Gly Val Arg Asn Ile Phe Pro Thr
65   70   75   80

Ala Ile Val Leu Phe Thr Leu Gly Ser Leu Phe Cys Ala Leu Ser Gly
                  85   90   95

Thr Leu Asn Glu Leu Leu Leu Ala Arg Ala Leu Gln Gly Val Gly Gly
            100   105   110

Ala Met Met Val Pro Val Gly Arg Leu Thr Val Met Lys Ile Val Pro
            115   120   125

Arg Glu Gln Tyr Met Ala Ala Met Thr Phe Val Thr Leu Pro Gly Gln
            130   135   140

Val Gly Pro Leu Leu Gly Pro Ala Leu Gly Gly Leu Leu Val Glu Tyr
145   150   155   160

Ala Ser Trp His Trp Ile Phe Leu Ile Asn Ile Pro Val Gly Ile Ile
                  165   170   175

Gly Ala Ile Ala Thr Leu Leu Leu Met Pro Asn Tyr Thr Met Gln Thr
            180   185   190

Arg Arg Phe Asp Leu Ser Gly Phe Leu Leu Leu Ala Val Gly Met Ala
            195   200   205

Val Leu Thr Leu Ala Leu Asp Gly Ser Lys Gly Thr Gly Leu Ser Pro
            210   215   220

Leu Thr Ile Ala Gly Leu Val Ala Val Gly Val Val Ala Leu Val Leu
225   230   235   240

Tyr Leu Leu His Ala Arg Asn Asn Asn Arg Ala Leu Phe Ser Leu Lys

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                    245                         250                         255
Leu Phe Arg Thr Arg Thr Phe Ser Leu Gly Leu Ala Gly Ser Phe Ala
                    260                         265                         270
Gly Arg Ile Gly Ser Gly Met Leu Pro Phe Met Thr Pro Val Phe Leu
                    275                         280                         285
Gln Ile Gly Leu Gly Phe Ser Pro Phe His Ala Gly Leu Met Met Ile
290                         295                         300
Pro Met Val Leu Gly Ser Met Gly Met Lys Arg Ile Val Val Gln Val
305                         310                         315
Val Asn Arg Phe Gly Tyr Arg Arg Val Leu Val Ala Thr Thr Leu Gly
                    320                         330                         335
Leu Ser Leu Val Thr Leu Leu Phe Met Thr Thr Ala Leu Leu Gly Trp
                    340                         345                         350
Tyr Tyr Val Leu Pro Phe Val Leu Phe Leu Gln Gly Met Val Asn Ser
                    355                         360                         365
Thr Arg Phe Ser Ser Met Asn Thr Leu Thr Leu Lys Asp Leu Pro Asp
                    370                         375                         380
Asn Leu Ala Ser Ser Gly Asn Ser Leu Leu Ser Met Ile Met Gln Leu
385                         390                         395                         400
Ser Met Ser Ile Gly Val Thr Ile Ala Gly Leu Leu Leu Gly Leu Phe
                    405                         410                         415
Gly Ser Gln His Val Ser Val Asp Ser Gly Thr Thr Gln Thr Val Phe
                    420                         425                         430
Met Tyr Thr Trp Leu Ser Met Ala Leu Ile Ile Ala Leu Pro Ala Phe
                    435                         440                         445
Ile Phe Ala Arg Val Pro Asn Asp Thr His Gln Asn Val Ala Ile Ser
450                         455                         460
Arg Arg Lys Arg Ser Ala Gln
465                         470
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<211> 185
<211> 344
<212> PRT
<213> E. Coli.

<400> 163
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                      1                       5                          10                          15
Met Gln Ile Arg Ile Met Leu Phe Ile Leu Met Met Met Val Met Pro
                      20                          25                          30
Val Ser Tyr Ala Ala Cys Tyr Ser Glu Leu Ser Val Gln His Asn Leu
35                          40                          45
Val Val Gln Gly Asp Phe Ala Leu Thr Gln Thr Gln Met Ala Thr Tyr
50                          55                          60
Gln His Asn Phe Asn Asp Ser Ser Cys Val Ser Thr Asn Thr Ile Thr
65                          70                          75                          80
Pro Met Ser Pro Ser Asp Ile Ile Val Gly Leu Tyr Asn Asp Thr Ile
                      85                          90                          95
Lys Leu Asn Leu His Phe Glu Trp Thr Asn Lys Asn Asn Ile Thr Leu
                      100                         105                         110
Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr
                      115                         120                         125
Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly
                      130                         135                         140
Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser
145                         150                         155                         160
Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly
```

Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln
                165   170   175
Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile
                180   185   190
Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile
                195   200   205
Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser
    210   215   220
Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln
    225   230   235   240
Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu
                    245   250   255
Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val
                260   265   270
Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile
                275   280   285
Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys
    290   295   300
Ser Lys Leu Thr Asp Thr Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr
    305   310   315   320
Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr
                325   330   335
Ala Leu Ile Asn Val Lys Tyr Asp
                340

    <211> 344
    <211> PRT
    <211> E. Coli

    <400> 346
Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu
  1   10   15
Gly Ile Glu Ala Tyr Ala Ala Glu Glu Thr Phe Asp Thr His Phe Met
                20   25   30
Ile Gly Gly Met Lys Asp Gln Gln Val Ala Asn Ile Arg Leu Asp Asp
                35   40   45
Asn Gln Pro Leu Pro Gly Gln Tyr Asp Ile Asp Ile Tyr Val Asn Lys
    50   55   60
Gln Trp Arg Gly Lys Tyr Glu Ile Ile Val Lys Asp Asn Pro Gln Glu
  65   70   75   80
Thr Cys Leu Ser Arg Glu Val Ile Lys Arg Leu Gly Ile Asn Ser Asp
                    85   90   95
Asn Phe Ala Ser Gly Lys Gln Cys Leu Thr Phe Glu Gln Leu Val Gln
                100   105   110
Gly Gly Ser Tyr Thr Trp Asp Ile Gly Val Phe Arg Leu Asp Phe Ser
                115   120   125
Val Pro Gln Ala Trp Val Glu Gln Leu Glu Ser Gly Tyr Val Pro Pro
    130   135   140
Glu Asn Trp Glu Arg Gly Ile Asn Ala Phe Tyr Thr Ser Tyr Tyr Leu
    145   150   155   160
Ser Gln Tyr Tyr Ser Asp Tyr Lys Ala Ser Gly Asn Asn Lys Ser Thr
                165   170   175
Tyr Val Arg Phe Asn Ser Gly Leu Asn Leu Leu Gly Trp Gln Leu His
                180   185   190
Ser Asp Ala Ser Phe Ser Lys Thr Asn Asn Asn Pro Gly Val Trp Lys

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              195                    200                    205
Ser Asn Thr Leu Tyr Leu Glu Arg Gly Phe Ala Gln Leu Leu Gly Thr
210
Leu Arg Val Gly Asp Met Tyr Thr Ser Ser Asp Ile Phe Asp Ser Val
225                 230                 235                 240
Arg Phe Arg Gly Val Arg Leu Phe Arg Asp Met Gln Met Leu Pro Asn
                 245                 250                 255
Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn
                 260                 265                 270
Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu
             275                 280                 285
Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly
         290                 295                 300
Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr
305                 310                 320
Thr Tyr Leu Val Pro Tyr Ala Ala Val Pro Asn Met Leu Gln Pro Gly
                 325                 330                 335
Val Ser Lys Tyr Asp Leu Ala Ala Gly Arg Ser His Ile Glu Gly Ala
             340                 345                 350
Ser Lys Gln Ser Asp Phe Val Gln Ala Gly Tyr Gln Tyr Gly Phe Asn
         355                 360                 365
Asn Leu Leu Thr Leu Tyr Gly Ser Met Val Ala Asn Asn Tyr Tyr
     370                 375                 380
Ala Phe Thr Leu Gly Ala Gly Trp Asn Thr Arg Ile Gly Ala Ile Ser
385                 390                 395                 400
Val Asp Ala Thr Lys Ser His Ser Lys Gln Asp Asn Gly Asp Val Phe
                 405                 410                 415
Asp Gly Gln Ser Tyr Gln Ile Ala Tyr Asn Lys Phe Val Ser Gln Thr
             420                 425                 430
Ser Thr Arg Phe Gly Leu Ala Ala Trp Arg Tyr Ser Ser Arg Asp Tyr
         435                 440                 445
Arg Thr Phe Asn Asp His Val Trp Ala Asn Asn Lys Asp Asn Tyr Arg
     450                 455                 460
Arg Asp Glu Asn Asp Val Tyr Asp Ile Ala Asp Tyr Tyr Gln Asn Asp
465                 470                 475                 480
Phe Gly Arg Lys Asn Ser Phe Ser Ala Asn Met Ser Gln Ser Leu Pro
                 485                 490                 495
Glu Gly Trp Gly Ser Val Ser Leu Ser Thr Leu Trp Arg Asp Tyr Trp
             500                 505                 510
Gly Arg Ser Gly Ser Ser Lys Asp Tyr Gln Leu Ser Tyr Ser Asn Asn
         515                 520                 525
Leu Arg Arg Ile Ser Tyr Thr Leu Ala Ala Ser Gln Ala Tyr Asp Glu
     530                 535                 540
Asn His His Glu Glu Lys Arg Phe Asn Ile Phe Ile Ser Ile Pro Phe
545                 550                 555                 560
Asp Trp Gly Asp Asp Val Ser Thr Pro Arg Arg Gln Ile Tyr Met Ser
                 565                 570                 575
Asn Ser Thr Thr Phe Asp Asp Gln Gly Phe Ala Ser Asn Asn Thr Gly
             580                 585                 591
Leu Ser Gly Thr Val Gly Ser Arg Asp Gln Phe Asn Tyr Gly Val Asn
         595                 600                 605
Leu Ser His Gln His Ser Gly Asn Glu Thr Thr Ala Gly Ala Asn Leu
     610                 615                 620
Thr Trp Asn Ala Pro Val Ala Thr Val Asn Gly Ser Tyr Ser Gln Ser
625                 630                 635                 640
Ser Thr Tyr Arg Gln Ala Gly Ala Ser Val Ser Gly Gly Ile Val Ala
                 645                 650                 655
```

Trp Ser Gly Gly Val Asn Leu Ala Asn Arg Leu Ser Glu Thr Phe Ala
　　　　　　　 660　　　　　　　　　　　 665　　　　　　　　　　 670
Val Met Asn Ala Pro Gly Ile Lys Asp Ala Tyr Val Asn Gly Gln Lys
　　　　　 675　　　　　　　　　　 680　　　　　　　　　　 685
Tyr Arg Thr Thr Asn Arg Asn Gly Val Val Ile Tyr Asp Gly Met Thr
　　　 690　　　　　　　　　　 695　　　　　　　　　 700
Pro Tyr Arg Glu Asn His Leu Met Leu Asp Val Ser Gln Ser Asp Ser
705　　　　　　　　　　　 710　　　　　　　　　　 715　　　　　　　　 720
Glu Ala Glu Leu Arg Gly Asn Arg Lys Ile Ala Ala Pro Tyr Arg Gly
　　　　　　　 725　　　　　　　　　 730　　　　　　　　　　 735
Ala Val Val Leu Val Asn Phe Asp Thr Asp Gln Arg Lys Pro Trp Phe
　　　　　 740　　　　　　　　　 745　　　　　　　　　　 750
Ile Lys Ala Leu Arg Ala Asp Gly Gln Ser Leu Thr Phe Gly Tyr Glu
　　　 755　　　　　　　　　 760　　　　　　　　　　 765
Val Asn Asp Ile His Gly His Asn Ile Gly Val Val Gly Gln Gly Ser
　　　 770　　　　　　　　　 775　　　　　　　　 780
Gln Leu Pro Ile Arg Thr Asn Glu Val Pro Pro Ser Val Asn Val Ala
785　　　　　　　　 790　　　　　　　　　 795　　　　　　　　 800
Ile Asp Lys Gln Gln Gly Leu Ser Cys Thr Ile Thr Phe Gly Lys Glu
　　　　　　　 805　　　　　　　　　 810　　　　　　　　　 815
Ile Asp Gln Ser Arg Asn Tyr Ile Cys Gln
　　　　　　 820　　　　　　　　 825

<210> 147
<211> 149
<211> PRT
<213> E. Coli

<400> 147

Met Ala Ala Ile Pro Trp Arg Pro Phe Asn Leu Arg Gly Ile Lys Met
1　　　　　　　 5　　　　　　　　　 10　　　　　　　　　 15
Lys Gly Leu Leu Ser Leu Leu Ile Phe Ser Met Val Leu Pro Ala His
　　　　　　　 15　　　　　　　　　 25　　　　　　　 30
Ala Gly Ile Val Ile Tyr Gly Thr Arg Ile Ile Tyr Pro Ala Glu Asn
　　　 35　　　　　　　　　 40　　　　　　　　　 45
Lys Glu Val Met Val Gln Leu Met Asn Gln Gly Asn Arg Ser Ser Leu
　　　 50　　　　　　　　 55　　　　　　　　　 60
Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys
65　　　　　　　　 70　　　　　　　　 75　　　　　　　　 80
Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala
　　　　　　 85　　　　　　　　 90　　　　　　　　　 95
Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro
　　　　　　 100　　　　　　　　 105　　　　　　　 110
Thr Asn Lys Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro
　　　 115　　　　　　　　 120　　　　　　　　　 125
Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Pro Ala Met Gln
　　　 130　　　　　　　　 135　　　　　　　　　 140
Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn
145　　　　　　　 150　　　　　　　　 155　　　　　　　　 160
Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu
　　　　　　 165　　　　　　　　 170　　　　　　　 171
Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys
　　　　　 180　　　　　　　　 185　　　　　　　 190
Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu
　　　　　 195　　　　　　　　 200　　　　　　　　 205
Glu Ser Gln Ser Val Asn Val Lys Ser Asn Asn Ala Asn Asn Trp His

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Leu Thr Ile Ile Asp Asp His Gly Asn Tyr Ile Ser Asp Lys Ile
225   230   235

<210> 185
<211> 182
<212> PRT
<213> E. Coli

<400> 185

Met Lys Arg Ser Ile Ile Ala Ala Ala Val Phe Ser Ser Phe Phe Met
 1   5   10   15
Ser Ala Gly Val Phe Ala Ala Asp Val Asp Thr Gly Thr Leu Thr Ile
                20   25   30
Lys Gly Asn Ile Ala Glu Ser Pro Cys Lys Phe Glu Ala Gly Gly Asp
                35   40   45
Ser Val Ser Ile Asn Met Pro Thr Val Pro Thr Ser Val Phe Glu Gly
                50   55   60
Lys Ala Lys Tyr Ser Thr Tyr Asp Asp Ala Val Gly Val Thr Ser Ser
65   70   75   80
Met Leu Lys Ile Ser Cys Pro Lys Glu Val Ala Gly Val Lys Leu Ser
                85   90   95
Leu Ile Thr Asn Asp Lys Ile Thr Gly Asn Asp Lys Ala Ile Ala Ser
                100   105   110
Ser Asn Asp Thr Val Gly Tyr Tyr Leu Tyr Leu Gly Asp Asn Ser Asp
                115   120   125
Val Leu Asp Val Ser Ala Pro Phe Asn Ile Glu Ser Tyr Lys Thr Ala
                130   135   140
Glu Gly Gln Tyr Ala Ile Pro Phe Lys Ala Lys Tyr Leu Lys Leu Thr
145   150   155   160
Asp Asn Ser Val Gln Ser Gly Asp Val Leu Ser Ser Leu Val Met Arg
                165   170   175
Val Ala Gln Asp

<210> 186
<211> 111
<212> PRT
<213> E. Coli

<400> 186

Met Ser Ser Glu Arg Asp Leu Val Asn Phe Leu Gly Asp Phe Ser Met
 1   5   10   15
Asp Val Ala Lys Ala Val Ile Ala Gly Gly Val Ala Thr Ala Ile Gly
                20   25   30
Ser Leu Ala Ser Phe Ala Cys Val Ser Phe Gly Pro Pro Val Ile Leu
                35   40   45
Val Gly Gly Ala Ile Leu Leu Thr Gly Ile Val Tyr Thr Val Val Leu
                50   55   60
Asn Gln Ile Asp Ala Gln Cys His Leu Ser Glu Lys Leu Lys Tyr Ala
65   70   75   80
Ile Arg Asp Gly Leu Lys Arg Gln Gln Glu Leu Asp Lys Trp Lys Arg
                85   90   95
Glu Asn Met Thr Pro Phe Met Tyr Val Leu Asn Thr Pro Pro Val Ile

100   105   110

```
Met Thr Asp Tyr Leu Leu Leu Phe Val Gly Thr Val Leu Val Asn Asn
1               5                   10                  15
Phe Val Leu Val Lys Phe Leu Gly Leu Cys Pro Phe Met Gly Val Ser
                20              25                  30
Lys Lys Leu Glu Thr Ala Met Gly Met Gly Leu Ala Thr Thr Phe Val
            35              40              45
Met Thr Leu Ala Ser Ile Cys Ala Trp Leu Ile Asp Thr Trp Ile Leu
    50              55              60
Ile Pro Leu Asn Leu Ile Tyr Leu Arg Thr Leu Ala Phe Ile Leu Val
65              70              75                  80
Ile Ala Val Val Val Gln Phe Thr Glu Met Val Val Arg Lys Thr Ser
                85              90                  95
Pro Val Leu Tyr Arg Leu Leu Gly Ile Phe Leu Pro Leu Ile Thr Thr
                100             105                 110
Asn Cys Ala Val Leu Gly Val Ala Leu Leu Asn Ile Asn Leu Gly His
            115             120                 125
Asn Phe Leu Gln Ser Ala Leu Tyr Gly Phe Ser Ala Ala Val Gly Phe
            130             135             140
Ser Leu Val Met Val Leu Phe Ala Ala Ile Arg Glu Arg Leu Ala Val
145             150             155                 160
Ala Asp Val Pro Ala Pro Phe Arg Gly Asn Ala Ile Ala Leu Ile Thr
                165             170             175
Ala Gly Leu Met Ser Leu Ala Phe Met Gly Phe Ser Gly Leu Val Lys
                180             185             190
Leu
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```
Met Asn Ala Ile Trp Ile Ala Val Ala Ala Val Ser Leu Leu Gly Leu
1               5                   10                  15
Ala Phe Gly Ala Ile Leu Gly Tyr Ala Ser Arg Arg Phe Ala Val Glu
                20              25                  30
Asp Asp Pro Val Val Glu Lys Ile Asp Glu Ile Leu Pro Gln Ser Gln
            35              40              45
Cys Gly Gln Cys Gly Tyr Pro Gly Cys Arg Pro Tyr Ala Glu Ala Ile
    50              55              60
Ser Cys Asn Gly Glu Lys Ile Asn Arg Cys Ala Pro Gly Gly Glu Ala
65              70              75                  80
Val Met Leu Lys Ile Ala Glu Leu Leu Asn Val Glu Pro Gln Pro Leu
                85              90                  95
Asp Gly Glu Ala Gln Glu Ile Thr Pro Ala Arg Met Val Ala Val Ile
```

```
                    100                   105                   110
Asp Glu Asn Asn Cys Ile Gly Cys Thr Lys Cys Ile Gln Ala Cys Pro
                115                   120                   125
Val Asp Ala Ile Val Gly Ala Thr Arg Ala Met His Thr Val Met Ser
            130                   135                   140
Asp Leu Cys Thr Gly Cys Asn Leu Cys Val Asp Pro Cys Pro Thr His
145                   150                   155                   160
Cys Ile Ser Leu Gln Pro Val Ala Glu Thr Pro Asp Ser Trp Lys Trp
                165                   170                   175
Asp Leu Asn Thr Ile Pro Val Arg Ile Ile Pro Val Glu His His Ala
            180                   185                   190


        <210> 28?
        <211> 30?
        <21.> PRT
        <21.> E. Coli

        <40.> 13?

Met Leu Lys Leu Phe Ser Ala Phe Arg Lys Asn Lys Ile Trp Asp Phe
1               5                   10                  15
Asn Gly Gly Ile His Pro Pro Glu Met Lys Thr Gln Ser Asn Gly Thr
                20                  25                  30
Pro Leu Asn Gln Val Pro Leu Ala Gln Arg Phe Val Ile Pro Leu Lys
            35                  40                  45
Gln His Ile Gly Ala Gly Gly Glu Leu Cys Val Ser Val Gly Asp Lys
        50                  55                  60
Val Leu Arg Gly Gln Pro Leu Thr Arg Gly Arg Gly Lys Met Leu Pro
65                  70                  75                  80
Val His Ala Pro Thr Ser Gly Thr Val Thr Ala Ile Ala Pro His Ser
                85                  90                  95
Thr Ala His Pro Ser Ala Leu Ala Glu Leu Ser Val Ile Ile Asp Ala
            100                 105                 111
Asp Gly Glu Asp Cys Trp Ile Pro Arg Asp Gly Trp Ala Asp Tyr Arg
            115                 120                 125
Thr Arg Ser Arg Glu Glu Leu Ile Glu Arg Ile His Gln Phe Gly Val
        130                 135                 140
Ala Gly Leu Gly Gly Ala Gly Phe Pro Thr Gly Val Lys Leu Gln Gly
145                 150                 155                 160
Gly Gly Asp Lys Ile Glu Thr Leu Ile Ile Asn Ala Ala Glu Cys Glu
                165                 170                 175
Pro Tyr Ile Thr Ala Asp Asp Arg Leu Met Gln Asp Cys Ala Ala Gln
            180                 185                 191
Val Val Glu Gly Ile Arg Ile Leu Ala His Ile Leu Gln Pro Arg Glu
            195                 200                 205
Ile Leu Ile Gly Ile Glu Asp Asn Lys Pro Gln Ala Ile Ser Met Leu
        210                 215                 220
Arg Ala Val Leu Ala Asp Ser Asn Asp Ile Ser Leu Arg Val Ile Pro
225                 230                 235                 240
Thr Lys Tyr Pro Ser Gly Gly Ala Lys Gln Leu Thr Tyr Ile Leu Thr
                245                 250                 255
Gly Lys Gln Val Pro His Gly Gly Arg Ser Ser Asp Ile Gly Val Leu
            260                 265                 270
Met Gln Asn Val Gly Thr Ala Tyr Ala Val Lys Arg Ala Val Ile Asp
            275                 280                 285
Gly Gln Pro Ile Thr Glu Arg Val Val Thr Leu Thr Gly Glu Ala Ile
290                 295                 300
```

Ala Arg Pro Gly Asn Val Trp Ala Arg Leu Gly Thr Pro Val Arg His
305 310 315 320
Leu Leu Asn Asp Ala Gly Phe Cys Pro Ser Ala Asp Gln Met Val Ile
325 330 335
Met Gly Gly Pro Leu Met Gly Phe Thr Leu Pro Trp Leu Asp Val Pro
340 345 350
Val Val Lys Ile Thr Asn Cys Leu Leu Ala Pro Ser Ala Asn Glu Leu
355 360 365
Gly Glu Pro Gln Glu Glu Gln Ser Cys Ile Arg Cys Ser Ala Cys Ala
370 375 380
Asp Ala Cys Pro Ala Asp Leu Leu Pro Gln Gln Leu Tyr Trp Phe Ser
385 390 395 400
Lys Gly Gln Gln His Asp Lys Ala Thr Thr His Asn Ile Ala Asp Cys
405 410 415
Ile Glu Cys Gly Ala Lys Ala Trp Val Cys Pro Ser Asn Ile Pro Leu
420 425 430
Val Gln Tyr Phe Arg Gln Glu Lys Ala Glu Ile Ala Ala Ile Arg Gln
435 440 445
Glu Glu Lys Arg Ala Ala Glu Ala Lys Ala Arg Phe Glu Ala Arg Gln
450 455 460
Ala Arg Leu Glu Arg Glu Lys Ala Ala Arg Leu Glu Arg His Lys Ser
465 470 475 480
Ala Ala Val Glu Pro Ala Ala Lys Asp Lys Asp Ala Ile Ala Ala Ala
485 490 495
Leu Ala Arg Val Lys Glu Lys Gln Ala Gln Ala Thr Gln Pro Ile Val
500 505 510
Ile Lys Ala Gly Glu Arg Pro Asp Asn Ser Ala Ile Ile Ala Ala Arg
515 520 525
Glu Ala Arg Lys Ala Gln Ala Arg Ala Lys Gln Ala Glu Leu Gln Gln
530 535 540
Thr Asn Asp Ala Ala Thr Val Ala Asp Pro Arg Lys Thr Ala Val Glu
545 550 555 560
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
565 570 575
Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
580 585 590
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
595 600 605
Asn Ala Glu Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Glu
610 615 620
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
625 630 635 640
Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
645 650 655
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Arg Glu Gln Gln Pro Ala
660 665 670
Asn Ala Glu Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Glu
675 680 685
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
690 695 700
Asn Ala Val Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Ala
705 710 715 720
Ala Ala Ile Ala Arg Ala Gln Ala Lys Lys Ala Ala Gln Gln Lys Val
725 730 735
Val Asn Glu Asp
740

<400> 193

```
Met Val Phe Arg Ile Ala Ser Ser Pro Tyr Thr His Asn Gln Arg Gln
1               5                   10                  15

Thr Ser Arg Ile Met Leu Leu Val Leu Leu Ala Ala Val Pro Gly Ile
            20                  25                  30

Ala Ala Gln Leu Trp Phe Phe Gly Trp Gly Thr Leu Val Gln Ile Leu
        35                  40                  45

Leu Ala Ser Val Ser Ala Leu Leu Ala Glu Ala Leu Val Leu Lys Leu
    50                  55                  60

Arg Lys Gln Ser Val Ala Ala Thr Leu Lys Asp Asn Ser Ala Leu Leu
65                  70                  75                  80

Thr Gly Leu Leu Leu Ala Val Ser Ile Pro Pro Leu Ala Pro Trp Trp
            85                  90                  95

Met Val Val Leu Gly Thr Val Phe Ala Val Ile Ile Ala Lys Gln Leu
            100                 105                 110

Tyr Gly Gly Leu Gly Gln Asn Pro Phe Asn Pro Ala Met Ile Gly Tyr
            115                 120                 125

Val Val Leu Leu Ile Ser Phe Pro Val Gln Met Thr Ser Trp Leu Pro
    130                 135                 140

Pro His Glu Ile Ala Val Asn Ile Pro Gly Phe Ile Asp Ala Ile Gln
145                 150                 155                 160

Val Ile Phe Ser Gly His Thr Ala Ser Gly Gly Asp Met Asn Thr Leu
                165                 170                 175

Arg Leu Gly Ile Asp Gly Ile Ser Gln Ala Thr Pro Leu Asp Thr Phe
            180                 185                 190

Lys Thr Ser Val Arg Ala Gly His Ser Val Glu Gln Ile Met Gln Tyr
            195                 200                 205

Pro Ile Tyr Ser Gly Ile Leu Ala Gly Ala Gly Trp Gln Trp Val Asn
        210                 215                 220

Leu Ala Trp Leu Ala Gly Gly Val Trp Leu Leu Trp Gln Lys Ala Ile
225                 230                 235                 240

Arg Trp His Ile Pro Leu Ser Phe Leu Val Thr Leu Ala Leu Cys Ala
                245                 250                 255

Met Leu Gly Trp Leu Phe Ser Pro Glu Thr Leu Ala Ala Pro Gln Ile
            260                 265                 270

His Leu Leu Ser Gly Ala Thr Met Leu Gly Ala Phe Phe Ile Leu Thr
            275                 280                 285

Asp Pro Val Thr Ala Ser Thr Thr Asn Arg Gly Arg Leu Ile Phe Gly
        290                 295                 300

Ala Leu Ala Gly Leu Leu Val Trp Leu Ile Arg Ser Phe Gly Gly Tyr
305                 310                 315                 320

Pro Asp Gly Val Ala Phe Ala Val Leu Leu Ala Asn Ile Thr Val Pro
                325                 330                 335

Leu Ile Asp Tyr Tyr Thr Arg Pro Arg Val Tyr Gly His Arg Lys Gly
            340                 345                 350
```

<400> 294

```
Met Leu Lys Thr Ile Arg Lys His Gly Ile Thr Leu Ala Leu Phe Ala
 1               5                  10              15
Ala Gly Ser Thr Gly Leu Thr Ala Ala Ile Asn Gln Met Thr Lys Thr
            20              25              30
Thr Ile Ala Glu Gln Ala Ser Leu Gln Gln Lys Ala Leu Phe Asp Gln
        35              40              45
Val Leu Pro Ala Glu Arg Tyr Asn Asn Ala Leu Ala Gln Ser Cys Tyr
    50              55              60
Leu Val Thr Ala Pro Glu Leu Gly Lys Gly Glu His Arg Val Tyr Ile
65              70              75              80
Ala Lys Gln Asp Asp Lys Pro Val Ala Ala Val Leu Glu Ala Thr Ala
                85              90              95
Pro Asp Gly Tyr Ser Gly Ala Ile Gln Leu Leu Val Gly Ala Asp Phe
            100             105             110
Asn Gly Thr Val Leu Gly Thr Arg Val Thr Glu His His Glu Thr Pro
        115             120             125
Gly Leu Gly Asp Lys Ile Glu Leu Arg Leu Ser Asp Trp Ile Thr His
    130             135             140
Phe Ala Gly Lys Lys Ile Ser Gly Ala Asp Asp Ala His Trp Ala Val
145             150             155             160
Lys Lys Asp Gly Gly Asp Phe Asp Gln Phe Thr Gly Ala Thr Ile Thr
                165             170             175
Pro Arg Ala Val Val Asn Ala Val Lys Arg Ala Gly Leu Tyr Ala Gln
            180             185             190
Thr Leu Pro Ala Gln Leu Ser Gln Leu Pro Ala Cys Gly Glu
    195             200             205
```

<210> 295
<211> 291
<212> PRT

<400> 295

```
Met Ser Glu Ile Lys Asp Val Ile Val Gln Gly Leu Trp Lys Asn Asn
 1               5                  11              15
Ser Ala Leu Val Gln Leu Leu Gly Leu Cys Pro Leu Leu Ala Val Thr
            20              25              30
Ser Thr Ala Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr Thr Leu Val
        35              40              45
Leu Thr Leu Thr Asn Leu Thr Ile Ser Thr Leu Arg His Trp Thr Pro
    50              55              60
Ala Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala Ser Val Val
65              70              75              80
Ser Ala Val Gln Met Leu Ile Asn Ala Tyr Ala Phe Gly Leu Tyr Gln
                85              90              95
Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys Ile Val Val
            100             105             110
Gly Arg Ala Glu Ala Phe Ala Ala Lys Lys Gly Pro Ala Leu Ser Ala
        115             120             125
Leu Asp Gly Phe Ser Ile Gly Met Gly Ala Thr Cys Ala Met Phe Val
    130             135             140
Leu Gly Ser Leu Arg Glu Ile Ile Gly Asn Gly Thr Leu Phe Asp Gly
145             150             155             160
```

```
Ala Asp Ala Leu Leu Gly Ser Trp Ala Lys Val Leu Arg Val Glu Ile
                165             170             175
Phe His Thr Asp Ser Pro Phe Leu Leu Ala Met Leu Pro Pro Gly Ala
                180             185             190
Phe Ile Gly Leu Gly Leu Met Leu Ala Gly Lys Tyr Leu Ile Asp Glu
                19.             200             205
Arg Met Lys Lys Arg Arg Ala Glu Ala Ala Ala Glu Arg Ala Leu Pro
        210             215             220
Asn Gly Glu Thr Gly Asn Val
225             230
```

```
 ·210· ·296
 ·211· ·711
 ·212· PRT
 ·213· H. Coli

 ·400· ·296
```

```
Met Asn Lys Ala Lys Arg Leu Glu Ile Leu Thr Arg Leu Arg Glu Asn
1                               10              15
Asn Pro His Pro Thr Thr Glu Leu Asn Phe Ser Ser Pro Phe Glu Leu
                20              25              30
Leu Ile Ala Val Leu Leu Ser Ala Gln Ala Thr Asp Val Ser Val Asn
        35              40              45
Lys Ala Thr Ala Lys Leu Tyr Pro Val Ala Asn Thr Pro Ala Ala Met
        50              55              60
Leu Glu Leu Gly Val Glu Gly Val Lys Thr Tyr Ile Lys Thr Ile Gly
65              70              75              80
Leu Tyr Asn Ser Lys Ala Glu Asn Ile Ile Lys Thr Cys Arg Ile Leu
                85              90              95
Leu Glu Gln His Asn Gly Glu Val Pro Glu Asp Arg Ala Ala Leu Glu
                100             105             110
Ala Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val Val Leu Asn Thr
                115             120             125
Ala Phe Gly Trp Pro Thr Ile Ala Val Asp Thr His Ile Phe Arg Val
        130             135             140
Cys Asn Arg Thr Gln Phe Ala Pro Gly Lys Asn Val Glu Gln Val Glu
145             150             155             160
Glu Lys Leu Leu Lys Val Val Pro Ala Glu Phe Lys Val Asp Cys His
                165             170             175
His Trp Leu Ile Leu His Gly Arg Tyr Thr Cys Ile Ala Arg Lys Pro
                180             185             190
Arg Cys Gly Ser Cys Ile Ile Glu Asp Leu Cys Glu Tyr Lys Glu Lys
        19.             200             205
Val Asp Ile
        210
```

```
 ·210· ·297
 ·211· 167
 ·212· PRT
 ·213· H. Coli

 ·400· ·297
```

```
Met Lys Arg Leu His Lys Arg Phe Leu Leu Ala Thr Phe Cys Ala Leu
1                               10              15
Phe Thr Ala Thr Leu Gln Ala Ala Asp Val Thr Ile Thr Val Asn Gly
```

```
                    10                      25                      30
Arg Val Val Ala Lys Pro Cys Thr Ile Gln Thr Lys Glu Ala Asn Val
        35                      40                      45
Asn Leu Gly Asp Leu Tyr Thr Arg Asn Leu Gln Gln Pro Gly Ser Ala
        50                      55                      60
Ser Gly Trp His Asn Ile Thr Leu Ser Leu Thr Asp Cys Pro Val Glu
65                      70                      75                      80
Thr Ser Ala Val Thr Ala Ile Val Thr Gly Ser Thr Asp Asn Thr Gly
                        85                      90                      95
Tyr Tyr Lys Asn Glu Gly Thr Ala Glu Asn Ile Gln Ile Glu Leu Arg
                100                     105                     110
Asp Asp Gln Asp Ala Ala Leu Lys Asn Gly Asp Ser Lys Thr Val Ile
        115                     120                     125
Val Asp Gly Ile Thr Arg Asn Ala Gln Phe Pro Leu Lys Ala Arg Ala
        130                     135                     140
Ile Thr Val Asn Gly Asn Ala Ser Gln Gly Thr Ile Glu Ala Leu Ile
145                     150                     155                     160
Asn Val Ile Tyr Thr Trp Gln
                165
```

```
Met Lys Tyr Asn Asn Ile Ile Phe Leu Gly Leu Cys Leu Gly Leu Thr
1                       5                       10                      15
Thr Tyr Ser Ala Leu Ser Ala Asp Ser Val Ile Lys Ile Ser Gly Arg
                20                      25                      30
Val Leu Asp Tyr Gly Cys Thr Val Ser Ser Asp Ser Leu Asn Phe Thr
                35                      40                      45
Val Asp Leu Gln Lys Asn Ser Ala Arg Gln Phe Pro Thr Thr Gly Ser
        51                      55                      60
Thr Ser Pro Ala Val Pro Phe Gln Ile Thr Leu Ser Glu Cys Ser Lys
65                      70                      75                      80
Gly Thr Thr Gly Val Arg Val Ala Phe Asn Gly Ile Glu Asp Ala Glu
                85                      90                      95
Asn Asn Thr Leu Leu Lys Leu Asp Glu Gly Ser Asn Thr Ala Ser Gly
                100                     105                     110
Leu Gly Ile Gln Ile Leu Asp Ala Asn Met Arg Pro Val Lys Leu Asn
        115                     120                     125
Asp Leu His Ala Gly Met Gln Trp Ile Pro Leu Val Pro Glu Gln Asn
        130                     135                     140
Asn Ile Leu Pro Tyr Ser Ala Arg Leu Lys Ser Thr Gln Lys Ser Val
145                     150                     155                     160
Asn Pro Gly Leu Val Arg Ala Ser Ala Thr Phe Thr Leu Glu Phe Gln
                165                     170                     175
```

```
Met Ser Gly Tyr Thr Val Lys Pro Pro Thr Gly Asp Thr Asn Glu Gln
1               5                   10                  15

Thr Gln Phe Ile Asp Tyr Phe Asn Leu Phe Tyr Ser Lys Arg Gly Gln
                20              25                  30

Glu Gln Ile Ser Ile Ser Gln Gln Leu Gly Asn Tyr Gly Thr Thr Phe
                35              40                  45

Phe Ser Ala Ser Arg Gln Ser Tyr Trp Asn Thr Ser Arg Ser Asp Gln
    50              55                  60

Gln Ile Ser Phe Gly Leu Asn Val Pro Phe Gly Asp Ile Thr Thr Ser
65                  70                  75                  80

Leu Asn Tyr Ser Tyr Ser Asn Asn Ile Trp Gln Asn Asp Arg Asp His
                85              90                  95

Leu Leu Ala Phe Thr Leu Asn Val Pro Phe Ser His Trp Met Arg Thr
                100             105                 110

Asp Ser Gln Ser Ala Phe Arg Asn Ser Asn Ala Ser Tyr Ser Met Ser
            115             120                 125

Asn Asp Leu Lys Gly Gly Met Thr Asn Leu Ser Gly Val Tyr Gly Thr
            130             135                 140

Leu Leu Pro Asp Asn Asn Leu Asn Tyr Ser Val Gln Val Gly Asn Thr
145             150                 155                 160

His Gly Gly Asn Thr Ser Ser Gly Thr Ser Gly Tyr Ser Ser Leu Asn
                165             170                 175

Tyr Arg Gly Ala Tyr Gly Asn Thr Asn Val Gly Tyr Ser Arg Ser Gly
                180             185                 190

Asp Ser Ser Gln Ile Tyr Tyr Gly Met Ser Gly Gly Ile Ile Ala His
            195             200                 205

Ala Asp Gly Ile Thr Phe Gly Gln Pro Leu Gly Asp Thr Met Val Leu
    210             215                 220

Val Lys Ala Pro Gly Ala Asp Asn Val Lys Ile Glu Asn Gln Thr Gly
225             230                 235                 240

Ile His Thr Asp Trp Arg Gly Tyr Ala Ile Leu Pro Phe Ala Thr Glu
                245             250                 255

Tyr Arg Gly Asn Arg Val Ala Leu Asn Ala Asn Ser Leu Ala Asp Asn
                260             265                 270

Val Glu Leu Asp Glu Thr Val Val Thr Val Ile Pro Thr His Gly Ala
            275             280                 285

Ile Ala Asn Ala Thr Phe Asn Ala Gln Ile Gly Gly Lys Val Leu Met
            290             295                 300

Thr Leu Lys Tyr Gly Asn Lys Ser Val Pro Phe Gly Ala Ile Val Thr
305             310                 315                 320

His Gly Glu Asn Lys Asn Gly Ser Ile Val Ala Glu Asn Gly Gln Val
                325             330                 335

Tyr Leu Thr Gly Leu Pro Gln Ser Gly Gln Leu Gln Val Ser Trp Gly
            340             345                 350

Lys Asp Lys Asn Ser Asn Cys Ile Val Glu Tyr Lys Leu Pro Glu Val
            355             360                 365

Ser Pro Gly Thr Leu Leu Asn Gln Gln Thr Ala Ile Cys Arg
370                 375                 380
```

```
Met Ile Ala Ile Ala Asp Ile Leu Gln Ala Gly Glu Lys Leu Thr Ala
1               5                   10                  15
Val Ala Pro Phe Leu Ala Gly Ile Gln Asn Glu Glu Gln Tyr Thr Gln
            20                  25                  30
Ala Leu Gly Leu Val Asp His Leu Leu Leu Asn Asp Pro Glu Asn Pro
        35                  40                  45
Leu Leu Asp Leu Val Cys Ala Lys Ile Thr Ala Trp Glu Glu Ser Ala
        50                  55                  60
Pro Glu Phe Ala Glu Phe Asn Ala Met Ala Gln Ala Met Pro Gly Gly
65                  70                  75                  80
Ile Ala Val Ile Arg Thr Leu Met Asp Gln Tyr Gly Leu Thr Leu Ser
                85                  90                  95
Asp Leu Pro Glu Ile Gly Ser Lys Ser Met Val Ser Arg Val Leu Ser
            100                 105                 110
Gly Lys Arg Lys Leu Thr Leu Glu His Ala Lys Lys Leu Ala Thr Arg
            115                 120                 125
Phe Gly Ile Ser Pro Ala Leu Phe Ile Asp
            130                 135
```

```
Met His Leu Ile Thr Gln Lys Ala Leu Lys Asp Ala Ala Glu Lys Tyr
1               5                   10                  15
Pro Gln His Lys Thr Glu Leu Val Ala Leu Gly Asn Thr Ile Ala Lys
            20                  25                  30
Gly Tyr Phe Lys Lys Pro Glu Ser Leu Lys Ala Val Phe Pro Ser Leu
        35                  40                  45
Asp Asn Pro Lys Tyr Leu Asp Lys His Tyr Val Phe Asn Val Gly Gly
        50                  55                  60
Asn Glu Leu Arg Val Val Ala Met Val Phe Phe Glu Ser Gln Lys Cys
65                  70                  75                  80
Tyr Ile Arg Glu Val Met Thr His Lys Glu Tyr Asp Phe Phe Thr Ala
                85                  90                  95
Val His Arg Thr Lys Gly Lys Lys
            100
```

```
Met Leu Ser Val Phe Thr Phe Phe Arg Cys Ala Arg Lys Gly Ala Phe
1               5                   10                  15
Met Leu Ala Arg Ser Gly Lys Val Ser Met Ala Thr Lys Lys Arg Ser
            20                  25                  30
Gly Glu Glu Ile Asn Asp Arg Gln Ile Leu Cys Gly Met Gly Ile Lys
        35                  40                  45
Leu Arg Arg Leu Thr Ala Gly Ile Cys Leu Ile Thr Gln Leu Ala Phe
```

```
          50                    55                    60
Pro Met Ala Ala Ala Ala Gln Gly Val Val Asn Ala Ala Thr Gln Gln
65                    70                    75                    80
Pro Val Pro Ala Gln Ile Ala Ile Ala Asn Ala Asn Thr Val Pro Tyr
                      85                    90                    95
Thr Leu Gly Ala Leu Glu Ser Ala Gln Ser Val Ala Glu Arg Phe Gly
                      100                   105                   110
Ile Ser Val Ala Glu Leu Arg Lys Leu Asn Gln Phe Arg Thr Phe Ala
                      115                   120                   125
Arg Ser Phe Asp Asn Val Arg Gln Gly Asp Glu Leu Asp Val Pro Ala
                      130                   135                   140
Gln Val Ser Glu Lys Lys Leu Thr Pro Pro Pro Gly Asn Ser Ser Asp
                      145                   150                   155       160
Asn Leu Glu Gln Gln Ile Ala Ser Thr Ser Gln Gln Ile Gly Ser Leu
                            165                   170                   175
Leu Ala Glu Asp Met Asn Ser Glu Gln Ala Ala Asn Met Ala Arg Gly
                      180                   185                   190
Trp Ala Ser Ser Gln Ala Ser Gly Ala Met Thr Asp Trp Leu Ser Arg
                      195                   200                   205
Phe Gly Thr Ala Arg Ile Thr Leu Gly Val Asp Glu Arg Pro Ser Leu
                      210                   215                   220
Lys Asn Ser Gln Phe Asp Phe Leu His Pro Trp Tyr Glu Thr Pro Asp
                            225                   230                   240
Asn Leu Phe Phe Ser Gln His Thr Leu His Arg Thr Arg Glu Arg Thr
                            245                   250                   255
Gln Ile Asn Asn Gly Leu Gly Trp Arg His Phe Thr Pro Thr Trp Met
                      260                   265                   270
Ser Gly Ile Asn Phe Phe Phe Asp His Asp Leu Ser Arg Tyr His Ser
                      275                   280                   285
Arg Ala Gly Ile Gly Ala Glu Tyr Trp Arg Asp Tyr Leu Lys Leu Ser
                      290                   295                   300
Ser Asn Gly Tyr Leu Arg Leu Thr Asn Trp Arg Ser Ala Pro Glu Leu
305                   310                   315                   320
Asp Asn Asp Tyr Glu Ala Arg Pro Ala Asn Gly Trp Arg Val Arg Ala
                            325                   330                   335
Glu Ser Trp Leu Pro Ala Trp Pro His Leu Gly Gly Lys Leu Val Tyr
                      340                   345                   350
Glu Gln Tyr Tyr Gly Asp Glu Val Ala Leu Phe Asp Lys Asp Asp Arg
                      355                   360                   365
Gln Ser Asn Pro His Ala Ile Thr Ala Gly Leu Asn Tyr Thr Pro Phe
                      370                   375                   380
Pro Leu Met Thr Phe Ser Ala Glu Gln Arg Gln Gly Lys Gln Gly Glu
385                   390                   395                   400
Asn Asp Thr Arg Phe Ala Val Asp Phe Thr Trp Gln Pro Gly Ser Ala
                      405                   410                   415
Met Gln Lys Gln Leu Asp Pro Asn Glu Val Ala Ala Arg Arg Ser Leu
                      420                   425                   430
Ala Gly Ser Arg Tyr Asp Leu Val Asp Arg Asn Asn Asn Ile Val Leu
                      435                   440                   445
Glu Tyr Arg Lys Lys Glu Leu Val Arg Leu Thr Leu Thr Asp Pro Val
                      450                   455                   460
Thr Gly Lys Ser Gly Glu Val Lys Ser Leu Val Ser Ser Leu Gln Thr
465                   470                   475                   480
Lys Tyr Ala Leu Lys Gly Tyr Asn Val Glu Ala Thr Ala Leu Glu Ala
                      485                   490                   495
Ala Gly Gly Lys Val Val Thr Thr Gly Lys Asp Ile Leu Val Thr Leu
                      500                   505                   510
```

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```
Pro Ala Tyr Arg Phe Thr Ser Thr Pro Glu Thr Asp Asn Thr Trp Pro
        515                 520              525
Ile Glu Val Thr Ala Glu Asp Val Lys Gly Asn Leu Ser Asn Arg Glu
        530             535             540
Gln Ser Met Val Val Val Gln Ala Pro Thr Leu Ser Gln Lys Asp Ser
545             550             555             560
Ser Val Ser Leu Ser Thr Gln Thr Leu Asn Ala Arg Ser His Ser Thr
            565             570             575
Ala Thr Leu Thr Phe Ile Ala His Asp Ala Ala Gly Asn Pro Val Val
            580             585             590
Gly Leu Val Leu Ser Thr Arg His Glu Gly Val Gln Asp Ile Thr Leu
        595             600             605
Ser Asp Trp Lys Asp Asn Gly Asp Gly Ser Tyr Thr Gln Ile Leu Thr
    610             615             620
Thr Gly Ala Met Ser Gly Thr Leu Thr Leu Met Pro Gln Leu Asn Gly
625             630             635             640
Val Asp Ala Ala Lys Ala Pro Ala Val Val Asn Ile Ile Ser Val Ser
            645             650             655
Ser Ser Arg Thr His Ser Ser Ile Lys Ile Asp Lys Asp Arg Tyr Leu
            660             665             670
Ser Gly Asn Pro Ile Glu Val Thr Val Glu Leu Arg Asp Glu Asn Asp
        675             680             685
Lys Pro Val Lys Glu Gln Lys Gln Gln Leu Asn Asn Ala Val Ser Ile
    690             695             700
Asp Asn Val Lys Pro Gly Val Thr Thr Asp Trp Lys Glu Thr Ala Asp
705             710             715             720
Gly Val Tyr Lys Ala Thr Tyr Thr Ala Tyr Thr Lys Gly Ser Gly Leu
            725             730             735
Thr Ala Lys Leu Leu Met Gln Asn Trp Asn Glu Asp Leu His Thr Ala
            740             745             750
Gly Phe Ile Ile Asp Ala Asn Pro Gln Ser Ala Lys Ile Ala Thr Leu
        755             760             765
Ser Ala Ser Asn Asn Gly Val Leu Ala Asn Glu Asn Ala Ala Asn Thr
    770             775             780
Val Ser Val Asn Val Ala Asp Glu Gly Ser Asn Pro Ile Asn Asp His
785             790             795             800
Thr Val Thr Phe Ala Val Leu Ser Gly Ser Ala Thr Ser Phe Asn Asn
            805             810             815
Gln Asn Thr Ala Lys Thr Arg Val Asn Gly Leu Ala Thr Phe Asp Leu
        820             825             830
Lys Ser Ser Lys Gln Glu Asp Asn Thr Val Glu Val Thr Leu Glu Asn
    835             840             845
Gly Val Lys Gln Thr Leu Ile Val Ser Phe Val Gly Asp Ser Ser Thr
855             860             865
Ala Gln Val Asp Leu Gln Lys Ser Lys Asn Glu Val Val Ala Asp Gly
870             875             880
Asn Asp Ser Val Thr Met Thr Ala Thr Val Arg Asp Ala Lys Gly Asn
            885             890             895
Leu Leu Asn Asp Val Met Val Thr Phe Asn Val Asn Ser Ala Glu Ala
        900             905             910
Lys Leu Ser Gln Thr Glu Val Asn Ser His Asp Gly Ile Ala Thr Ala
    915             920             925
Thr Leu Thr Ser Leu Lys Asn Gly Asp Tyr Arg Val Thr Ala Ser Val
    930             935             940
Ser Ser Gly Ser Gln Ala Asn Gln Gln Val Asn Phe Ile Gly Asp Gly
945             950             955             960
Ser Thr Ala Ala Leu Thr Leu Ser Val Pro Ser Gly Asp Ile Thr Val
```

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```
                965                    970                    975
Thr Asn Thr Ala Pro Gln Tyr Met Thr Ala Thr Leu Gln Asp Lys Asn
            980                    985                    990
Gly Asn Pro Leu Lys Asp Lys Glu Ile Thr Phe Ser Val Pro Asn Asp
            995                   1000                   1005
Val Ala Ser Lys Phe Ser Ile Ser Asn Gly Gly Lys Gly Met Thr Asp
      1010                   1015                   1020
Ser Asn Gly Val Ala Ile Ala Ser Leu Thr Gly Thr Leu Ala Gly Thr
1025                   1030                   1035                   1040
His Met Ile Met Ala Arg Leu Ala Asn Ser Asn Val Ser Asp Ala Gln
            1045                   1050                   1055
Pro Met Thr Phe Val Ala Asp Lys Asp Arg Ala Val Val Val Leu Gln
            1060                   1065                   1070
Thr Ser Lys Ala Glu Ile Ile Gly Asn Gly Val Asp Glu Thr Thr Leu
         1075                   1080                   1085
Thr Ala Thr Val Lys Asp Pro Ser Asn His Pro Val Ala Gly Ile Thr
         1090                   1095                   1100
Val Asn Phe Thr Met Pro Gln Asp Val Ala Ala Asn Phe Thr Leu Glu
1105                   1110                   1115                   1120
Asn Asn Gly Ile Ala Ile Thr Gln Ala Asn Gly Glu Ala His Val Thr
            1125                   1130                   1135
Leu Lys Gly Lys Lys Ala Gly Thr His Thr Val Thr Ala Thr Leu Gly
            1140                   1145                   1150
Asn Asn Asn Thr Ser Asp Ser Gln Pro Val Thr Phe Val Ala Asp Lys
            1155                   1160                   1165
Ala Ser Ala Gln Val Val Leu Gln Ile Ser Lys Asp Glu Ile Thr Gly
         1170                   1175                   1180
Asn Gly Val Asp Ser Ala Thr Leu Thr Ala Thr Val Lys Asp Gln Phe
1185                   1190                   1195                   1200
Asp Asn Glu Val Asn Asn Leu Pro Val Thr Phe Ser Ser Ala Ser Ser
            1205                   1210                   1215
Gly Leu Thr Leu Thr Pro Gly Val Ser Asn Thr Asn Glu Ser Gly Ile
            1220                   1225                   1230
Ala Gln Ala Thr Leu Ala Gly Val Ala Phe Gly Glu Lys Thr Val Thr
         1235                   1240                   1245
Ala Ser Leu Ala Asn Asn Gly Ala Ser Asp Asn Lys Thr Val His Phe
         1250                   1255                   1260
Ile Gly Asp Thr Ala Ala Ala Lys Ile Ile Glu Leu Ala Pro Val Pro
1265                   1270                   1275                   1280
Asp Ser Ile Ile Ala Gly Thr Pro Gln Asn Ser Ser Gly Ser Val Ile
            1285                   1290                   1295
Thr Ala Thr Val Val Asp Asn Asn Gly Phe Pro Val Lys Gly Val Thr
         1300                   1305                   1310
Val Asn Phe Thr Ser Asn Ala Ala Thr Ala Glu Met Thr Asn Gly Gly
         1315                   1320                   1325
Gln Ala Val Thr Asn Glu Gln Gly Lys Ala Thr Val Thr Tyr Thr Asn
         1330                   1335                   1340
Thr Arg Ser Ser Ile Glu Ser Gly Ala Arg Pro Asp Thr Val Glu Ala
1345                   1350                   1355                   1360
Ser Leu Glu Asn Gly Ser Ser Thr Leu Ser Thr Ser Ile Asn Val Asn
            1365                   1370                   1375
Ala Asp Ala Ser Thr Ala His Leu Thr Leu Leu Gln Ala Leu Phe Asp
         1380                   1385                   1390
Thr Val Ser Ala Gly Glu Thr Thr Ser Leu Tyr Ile Glu Val Lys Asp
         1395                   1410                   1415
Asn Tyr Gly Asn Gly Val Pro Gln Gln Glu Val Thr Leu Ser Val Ser
      1410                   1415                   1420
```

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Pro Ser Glu Gly Val Thr Pro Ser Asn Asn Ala Ile Tyr Thr Thr Asn
1425   1430   1435   1440

His Asp Gly Asn Phe Tyr Ala Ser Phe Thr Ala Thr Lys Ala Gly Val
                1445   1450   1455

Tyr Gln Leu Thr Ala Thr Leu Glu Asn Gly Asp Ser Met Gln Gln Thr
                1460   1465   1470

Val Thr Tyr Val Pro Asn Val Ala Asn Ala Glu Ile Thr Leu Ala Ala
                1475   1480   1485

Ser Lys Asp Pro Val Ile Ala Asp Asn Asn Asp Leu Thr Thr Leu Thr
            1490   1495   1500

Ala Thr Val Ala Asp Thr Glu Gly Asn Ala Ile Ala Asn Thr Glu Val
1505   1510   1515   1520

Thr Phe Thr Leu Pro Glu Asp Val Lys Ala Asn Phe Thr Leu Ser Asp
                1525   1530   1535

Gly Gly Lys Val Ile Thr Asp Ala Glu Gly Lys Ala Lys Val Thr Leu
                1540   1545   1550

Lys Gly Thr Lys Ala Gly Ala His Thr Val Thr Ala Ser Met Thr Gly
            1555   1560   1565

Gly Lys Ser Glu Gln Leu Val Val Asn Phe Ile Ala Asp Thr Leu Thr
        1570   1575   1580

Ala Gln Val Asn Leu Asn Val Thr Glu Asp Asn Phe Ile Ala Asn Asn
1585   1590   1595   1600

Val Gly Met Thr Arg Leu Gln Ala Thr Val Thr Asp Gly Asn Gly Asn
                1605   1610   1615

Pro Leu Ala Asn Glu Ala Val Thr Phe Thr Leu Pro Ala Asp Val Ser
                1620   16 5   1630

Ala Ser Phe Thr Leu Gly Gln Gly Gly Ser Ala Ile Thr Asp Ile Asn
                1635   1640   1645

Gly Lys Ala Glu Val Thr Leu Ser Gly Thr Lys Ser Gly Thr Tyr Pro
            1650   1655   1660

Val Thr Val Ser Val Asn Asn Tyr Gly Val Ser Asp Thr Lys Gln Val
1665   1670   1675   1680

Thr Leu Ile Ala Asp Ala Gly Thr Ala Lys Leu Ala Ser Leu Thr Ser
                1685   1690   1695

Val Tyr Ser Phe Val Val Ser Thr Thr Glu Gly Ala Thr Met Thr Ala
            1700   1705   1710

Ser Val Thr Arg Ala Asn Gly Asn Pro Val Glu Gly Ile Lys Val Asn
            1715   1720   1725

Phe Arg Gly Thr Ser Val Thr Leu Ser Ser Thr Ser Val Glu Thr Asp
        1730   1735   1740

Asp Arg Gly Phe Ala Glu Ile Leu Val Thr Ser Thr Glu Val Gly Leu
1745   1750   1755   1760

Lys Thr Val Ser Ala Ser Leu Ala Asp Lys Pro Thr Glu Val Ile Ser
            1765   1770   1775

Arg Leu Leu Asn Ala Ser Ala Asp Val Asn Ser Ala Thr Ile Thr Ser
            1780   1785   1790

Leu Glu Ile Pro Glu Gly Gln Val Met Val Ala Gln Asp Val Ala Val
        1795   1800   1805

Lys Ala His Val Asn Asp Gln Phe Gly Asn Pro Val Ala His Gln Pro
        1810   1815   1820

Val Thr Phe Ser Ala Glu Pro Ser Ser Gln Met Ile Ile Ser Gln Asn
1825   1830   1835   1840

Thr Val Ser Thr Asn Thr Gln Gly Val Ala Glu Val Thr Met Thr Pro
                1845   1850   1855

Glu Arg Asn Gly Ser Tyr Met Val Lys Ala Ser Leu Pro Asn Gly Ala
            1860   1865   1870

Ser Leu Glu Lys Gln Leu Glu Ala Ile Asp Glu Lys Leu Thr Leu Thr

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        1975              1380              1985
Ala Ser Ser Pro Leu Ile Gly Val Tyr Ala Pro Thr Gly Ala Thr Leu
     1890              1895              1900
Thr Ala Thr Leu Thr Ser Ala Asn Gly Thr Pro Val Glu Gly Gln Val
1405              1910              1915              1920
Ile Asn Phe Ser Val Thr Pro Glu Gly Ala Thr Leu Ser Gly Gly Lys
          1925              1930              1935
Val Arg Thr Asn Ser Ser Gly Gln Ala Pro Val Val Leu Thr Ser Asn
     1940              1945              1950
Lys Val Gly Thr Tyr Thr Val Thr Ala Ser Phe His Asn Gly Val Thr
     1955              1960              1965
Ile Gln Thr Gln Thr Thr Val Lys Val Phe Gly Asn Ser Ser Thr Ala
     1970              1975              1990
His Val Ala Ser Phe Ile Ala Asp Pro Ser Thr Ile Ala Ala Thr Asn
1985              1990              1995              2000
Thr Asp Leu Ser Thr Leu Lys Ala Thr Val Glu Asp Gly Ser Gly Asn
               2005              2010              2015
Leu Ile Glu Gly Leu Thr Val Tyr Phe Ala Leu Lys Ser Gly Ser Ala
          2020              2025              2030
Thr Leu Thr Ser Leu Thr Ala Val Thr Asp Gln Asn Gly Ile Ala Thr
     2035              2040              2045
Thr Ser Val Lys Gly Ala Met Thr Gly Ser Val Thr Val Ser Ala Val
     2050              2055              2060
Thr Thr Ala Gly Gly Met Gln Thr Val Asp Ile Thr Leu Val Ala Gly
2065              2070              2075              2080
Pro Ala Asp Thr Ser Gln Ser Val Leu Lys Ser Asn Arg Ser Ser Leu
               2085              2090              2095
Lys Gly Asp Tyr Thr Asp Ser Ala Glu Leu Arg Leu Val Leu His Asp
          2100              2105              2110
Ile Ser Gly Asn Pro Ile Lys Val Ser Glu Gly Met Gln Phe Val Gln
     2115              2120              2125
Ser Gly Thr Asn Val Pro Tyr Ile Lys Ile Ser Ala Ile Asp Tyr Ser
     2130              2135              2140
Leu Asn Ile Asn Gly Asp Tyr Lys Ala Thr Val Thr Gly Gly Gly Glu
2145              2150              2155              2160
Gly Ile Ala Thr Leu Ile Pro Val Leu Asn Gly Val His Gln Ala Gly
               2165              2170              2175
Leu Ser Thr Thr Ile Gln Phe Thr Arg Ala Glu Asp Lys Ile Met Ser
          2180              2185              2190
Gly Thr Val Ser Val Asn Gly Thr Asp Leu Pro Thr Thr Thr Phe Pro
     2195              2200              2205
Ser Gln Gly Pro Thr Gly Ala Tyr Tyr Gln Leu Asn Asn Asp Asn Phe
     2210              2215              2220
Ala Pro Gly Lys Thr Ala Ala Asp Tyr Glu Phe Ser Ser Ser Ala Ser
2225              2230              2235              2240
Trp Val Asp Val Asp Ala Thr Gly Lys Val Thr Phe Lys Asn Val Gly
               2245              2250              2255
Ser Asn Ser Glu Arg Ile Thr Ala Thr Pro Lys Ser Gly Gly Pro Ser
          2260              2265              2270
Tyr Val Tyr Glu Ile Arg Val Lys Ser Trp Trp Val Asn Ala Gly Gln
     2275              2280              2285
Ala Phe Met Ile Tyr Ser Leu Ala Glu Asn Phe Cys Ser Ser Asn Gly
     2290              2295              2300
Tyr Thr Leu Pro Arg Ala Asn Tyr Leu Asn His Cys Ser Ser Arg Gly
2515              2510              2315              2320
Ile Gly Ser Leu Tyr Ser Glu Trp Gly Asp Met Gly His Tyr Thr Thr
               2325              2330              2335
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Asp Ala Gly Phe Gln Ser Asn Met Tyr Trp Ser Ser Ser Pro Ala Asn
          2340   2345   2350

Ser Ser Glu Gln Tyr Val Val Ser Leu Ala Thr Gly Asp Gln Ser Val
          2355   2360   2365

Phe Glu Lys Leu Gly Phe Ala Tyr Ala Thr Cys Tyr Lys Asn Leu
          2370   2375   2380

          (211) 363
          (211) 61
          (21.) PRT
          (213) E. Coli

          (400) 363

Met Ser Lys Gly Ala Leu Tyr Glu Phe Asn Asn Pro Asp Gln Leu Lys
 1   5   10   15

Ile Pro Leu Pro His Lys His Ile Ala Ser Thr Phe Asn Asp Ile Met
          20   25   30

Ser Lys Asp Val Gly Tyr Ala Tyr Val Ser Leu Leu Tyr Ala Cys Pro
          35   40   45

Leu Lys Thr His Ser Leu Arg Leu Asn Pro Phe Ser Lys
          50   55   60

          (211) 364
          (211) 193
          (21.) PRT
          (213) E. Coli

          400 364

Met Gln Val Ala Glu Gln Arg Ile Gln Leu Ala Glu Ala Gln Ala Lys
 1   5   10   15

Ala Val Ala Thr Gln Asp Gly Pro Gln Ile Asp Phe Ser Ala Asp Met
          20   25   30

Glu Arg Gln Lys Met Ser Ala Glu Gly Leu Met Gly Pro Phe Ala Leu
          35   40   45

Asn Asp Pro Ala Ala Gly Thr Thr Gly Pro Trp Tyr Thr Asn Gly Thr
          50   55   60

Phe Gly Leu Thr Ala Gly Trp His Leu Asp Ile Trp Gly Lys Asn Arg
 65   70   75   80

Ala Glu Val Thr Ala Arg Leu Gly Thr Val Lys Ala Arg Ala Ala Glu
          85   90   95

Arg Glu Gln Thr Arg Gln Leu Leu Ala Gly Ser Val Ala Arg Leu Tyr
          100   105   110

Trp Glu Trp Gln Thr Gln Ala Ala Leu Asn Thr Val Leu Gln Gln Ile
          115   120   125

Glu Lys Glu Gln Asn Thr Ile Ile Ala Thr Asp Arg Gln Leu Tyr Gln
          130   135   140

Asn Gly Ile Thr Ser Ser Val Glu Gly Val Glu Thr Asp Ile Asn Ala
 145   150   155   160

Ser Lys Thr Arg Gln Gln Leu Asn Asp Val Ala Gly Lys Met Lys Ile
                    165   170   175

Ile Glu Ala Arg Leu Ser Ala Leu Thr Asn Asn Gln Thr Lys Ser Leu
          180   185   190

Lys Leu Lys Pro Val Ala Leu Pro Lys Val Ala Ser Gln Leu Pro Asp
          195   200   205

Glu Leu Gly Tyr Ser Leu Leu Ala Arg Arg Ala Asp Leu Gln Ala Ala

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      210                215                220
His Trp Tyr Val Glu Ser Ser Leu Ser Thr Ile Asp Ala Ala Lys Ala
225                230                235                240
Ala Phe Tyr Pro Asp Ile Asn Leu Met Ala Phe Leu Gln Gln Asp Ala
                245                250                255
Leu His Leu Ser Asp Leu Phe Arg His Ser Ala Gln Gln Met Gly Val
             260                265                270
Thr Ala Gly Leu Thr Leu Pro Ile Phe Asp Ser Gly Arg Leu Asn Ala
          275                280                285
Asn Leu Asp Ile Ala Lys Ala Glu Ser Asn Leu Ser Ile Ala Ser Tyr
       290                295                300
Asn Lys Ala Val Val Glu Ala Val Asn Asp Val Ala Arg Ala Ala Ser
305                310                315                320
Gln Val Gln Thr Leu Ala Glu Lys Asn Gln His Gln Ala Gln Ile Glu
                325                330                335
Arg Asp Ala Leu Arg Val Val Gly Leu Ala Gln Ala Arg Phe Asn Ala
             340                345                350
Gly Ile Ile Ala Gly Ser Arg Val Ser Glu Ala Arg Ile Pro Ala Leu
          355                360                365
Arg Glu Arg Ala Asn Gly Leu Leu Leu Gln Gly Gln Trp Leu Asp Ala
       370                375                380
Ser Ile Gln Leu Thr Gly Ala Leu Gly Gly Gly Tyr Lys Arg
385                390                395
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<211> 395
<212> PRT
<213> E. Coli

<210> ...

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Met Tyr Tyr His Ala Lys Leu Lys Asn Ile Ser Gln His Thr Val Ile
1                5                10                15
Ser Ala His Leu Phe Leu Pro Asp Tyr Ser Pro Met Asn Arg Asp Ser
             20                25                30
Phe Tyr Pro Ala Ile Ala Cys Phe Pro Leu Leu Leu Met Leu Ala Gly
          35                40                45
Cys Ala Pro Met His Glu Thr Arg Gln Ala Leu Ser Gln Gln Thr Pro
       50                55                60
Ala Ala Gln Val Asp Thr Ala Leu Pro Thr Ala Leu Lys Met Val Gly
75                70                75                80
Gln Thr Ala Asn Gly Gly Trp Ser Ile Thr Ile Ile Asn Ser Leu Pro
             85                90                95
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<211> 96
<212> PRT
<213> E. Coli

<210> ...

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Met Arg Val Leu Leu Ala Pro Met Glu Gly Val Leu Asp Ser Leu Val
1                5                10                15
Arg Glu Leu Leu Thr Glu Val Asn Asp Tyr Asp Leu Cys Ile Thr Glu
             20                25                30
Phe Val Arg Val Val Asp Gln Leu Leu Pro Val Lys Val Phe His Arg
          35                40                45
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Ile Cys Pro Glu Leu Gln Asn Ala Ser Arg Thr Pro Ser Gly Thr Leu
50   55   60

Val Arg Val Gln Leu Leu Gly Gln Phe Pro Gln Trp Leu Ala Glu Asn
65   70   75   80

Ala Ala Arg Ala Val Glu Leu Gly Ser Trp Gly Val Asp Leu Asn Cys
            85   90   95

Gly Cys Pro Ser Lys Thr Val Asn Gly Ser Gly Gly Gly Ala Thr Leu
            100   105   110

Leu Lys Asp Pro Glu Leu Ile Tyr Gln Gly Ala Lys Ala Met Arg Glu
        115   120   125

Ala Val Pro Ala His Leu Pro Val Ser Val Lys Val Arg Leu Gly Trp
        130   135   140

Asp Ser Gly Glu Lys Lys Phe Glu Ile Ala Asp Ala Val Gln Gln Ala
145   150   155   160

Gly Ala Thr Glu Leu Val Val His Gly Arg Thr Lys Glu Gln Gly Tyr
                165   170   175

Arg Ala Glu His Ile Asp Trp Gln Ala Ile Gly Asp Ile Arg Gln Arg
            180   185   190

Leu Asn Ile Pro Val Ile Ala Asn Gly Glu Ile Trp Asp Trp Gln Ser
        195   200   205

Ala Gln Gln Cys Met Ala Ile Ser Gly Cys Asp Ala Val Met Ile Gly
    210   215   220

Arg Gly Ala Leu Asn Ile Pro Asn Leu Ser Arg Val Val Lys Tyr Asn
225   230   235   240

Glu Pro Arg Met Pro Trp Pro Glu Val Val Ala Leu Leu Gln Lys Tyr
            245   250   255

Thr Arg Leu Glu Lys Gln Gly Asp Thr Gly Leu Tyr His Val Ala Arg
            260   265   270

Ile Lys Gln Trp Leu Ser Tyr Leu Arg Lys Glu Tyr Asp Glu Ala Thr
        275   280   285

Glu Leu Phe Gln His Val Arg Val Leu Asn Asn Ser Pro Asp Ile Ala
    290   295   300

Arg Ala Ile Gln Ala Ile Asp Ile Glu Lys Leu
305   310   315

<210> 207
<211> 796
<212> PRT
<213> E. Coli

<400> 207

Met Thr Ile Ser Thr Thr Ser Thr Pro His Asp Ala Val Phe Lys Ser
1   5   10   15

Phe Leu Arg His Pro Asp Thr Ala Arg Asp Phe Ile Asp Ile His Leu
        20   25   30

Pro Ala Pro Leu Arg Lys Leu Cys Asp Leu Thr Thr Leu Lys Leu Glu
    35   40   45

Pro Asn Ser Phe Ile Asp Glu Asp Leu Arg Gln Tyr Tyr Ser Asp Leu
50   55   60

Leu Trp Ser Val Lys Thr Gln Glu Gly Val Gly Tyr Ile Tyr Val Val
65   70   75   80

Ile Glu His Gln Ser Lys Pro Glu Glu Leu Met Ala Phe Arg Met Met
            85   90   95

Arg Tyr Ser Ile Ala Ala Met Gln Asn His Leu Asp Ala Gly Tyr Lys
            100   105   110

Glu Leu Pro Leu Val Leu Pro Met Leu Phe Tyr His Gly Cys Arg Ser

195   200   205
Glu Gly Thr Val Val Ala Ile Thr His Asp Arg Tyr Phe Leu Asp Asn
    210   215   220
Val Ala Gly Trp Ile Leu Glu Leu Asp Arg Gly Glu Gly Ile Pro Trp
225   230   235   240
Glu Gly Asn Tyr Ser Ser Trp Leu Glu Gln Lys Asp Gln Arg Leu Ala
                245   250   255
Gln Glu Ala Ser Gln Glu Ala Ala Arg Arg Lys Ser Ile Glu Lys Glu
                260   265   270
Leu Glu Trp Val Arg Gln Gly Thr Lys Gly Arg Gln Ser Lys Gly Lys
            275   280   285
Ala Arg Leu Ala Arg Phe Glu Glu Leu Asn Ser Thr Glu Tyr Gln Lys
            290   295   300
Arg Asn Gly Thr Asn Glu Leu Phe Ile Pro Pro Gly Pro Arg Leu Gly
305   310   315   320
Asp Lys Val Leu Glu Val Ser Asn Leu Arg Lys Ser Tyr Gly Asp Arg
                325   330   335
Leu Leu Ile Asp Asp Leu Ser Phe Ser Ile Pro Lys Gly Ala Ile Val
            340   345   350
Gly Ile Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Phe Arg Met
            355   360   365
Ile Ser Gly Gln Glu Gln Pro Asp Ser Gly Thr Ile Thr Leu Gly Glu
        370   375   380
Thr Val Lys Leu Ala Ser Val Asp Gln Phe Arg Asp Ser Met Asp Asn
385   390   395   400
Ser Lys Thr Val Trp Glu Glu Val Ser Gly Gly Leu Asp Ile Met Lys
                405   410   415
Ile Gly Asn Thr Glu Met Pro Ser Arg Ala Tyr Val Gly Arg Phe Asn
            420   425   430
Phe Lys Gly Val Asp Gln Gly Lys Arg Val Gly Glu Leu Ser Gly Gly
            435   440   445
Glu Arg Gly Arg Leu His Leu Ala Lys Leu Leu Gln Val Gly Gly Asn
        450   455   460
Met Leu Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Glu Thr Leu
465   470   475   480
Arg Ala Leu Glu Asn Ala Leu Leu Glu Phe Pro Gly Cys Ala Met Val
                485   490   495
Ile Ser His Asp Arg Trp Phe Leu Asp Arg Ile Ala Thr His Ile Leu
                500   505   510
Asp Tyr Gln Asp Glu Gly Lys Val Glu Phe Phe Glu Gly Asn Phe Thr
            515   520   525
Glu Tyr Glu Glu Tyr Lys Lys Arg Thr Leu Gly Ala Asp Ala Leu Glu
        530   535   540
Pro Lys Arg Ile Lys Tyr Lys Arg Ile Ala Lys
545   550

    <210> 309
    <211> 173
    <212> PRT
    <213> E. Coli

    <400> 309
Met Ser Lys Pro Lys Tyr Pro Phe Glu Lys Arg Leu Glu Val Val Asn
    1   5   10   15
His Tyr Phe Thr Thr Asp Asp Gly Tyr Arg Ile Ile Ser Ala Arg Phe

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          20   25   30

Gly Val Pro Arg Thr Gln Val Arg Thr Trp Val Ala Leu Tyr Glu Lys

          35   40   45

His Gly Glu Lys Gly Leu Ile Pro Lys Pro Lys Gly Val Ser Ala Asp

 50   55   60

Pro Glu Leu Arg Ile Lys Val Val Lys Ala Val Ile Glu Gln His Met

65   70   75   80

Ser Leu Asn Gln Ala Ala Ala His Phe Met Leu Ala Gly Ser Gly Ser

          85   90   95

Val Ala Arg Trp Leu Lys Val Tyr Glu Glu Arg Gly Glu Ala Gly Leu

Arg Ala Leu Lys Ile Gly Thr Lys Arg Asn Ile Ala Ile Ser Val Asp

          115   120   125

Pro Glu Lys Ala Ala Ser Ala Leu Glu Leu Ser Lys Asp Arg Arg Ile

          130   135   140

Glu Asp Leu Glu Arg Gln Val Arg Phe Leu Glu Thr Arg Leu Met Tyr

145   150   155   160

Leu Lys Lys Leu Lys Ala Leu Ala His Pro Thr Lys Lys

          165   170

      (211) ...
      (211) ...
      (212) PRT
      (213) E. Coli

      (411) ...

Met Lys Val Leu Asn Glu Leu Arg Gln Phe Tyr Pro Leu Asp Glu Leu
1   5   10   15

Leu Arg Ala Ala Glu Ile Pro Arg Ser Thr Phe Tyr Tyr His Leu Lys

          20   25   30

Ala Leu Ser Lys Pro Asp Lys Tyr Ala Asp Val Lys Lys Arg Ile Ser

          35   40   45

Glu Ile Tyr His Glu Asn Arg Gly Arg Tyr Gly Tyr Arg Arg Val Thr

          50   55   60

Leu Ser Leu His Arg Glu Gly Lys Gln Ile Asn His Lys Ala Val Gln

          65   70   75   80

Arg Leu Met Gly Thr Leu Ser Leu Lys Ala Ala Ile Lys Val Lys Arg

          85   90   95

Tyr Arg Ser Tyr Arg Gly Glu Val Gly Gln Thr Ala Pro Asn Val Leu

          100   105   110

Gln Arg Asp Phe Lys Ala Thr Arg Pro Asn Glu Lys Trp Val Thr Asp

          115   120   125

Val Thr Glu Phe Ala Val Asn Gly Arg Lys Leu Tyr Leu Ser Pro Val

          130   135   140

Ile Asp Leu Phe Asn Asn Glu Val Ile Ser Tyr Ser Leu Ser Glu Arg

145   150   155   160

Pro Val Met Asn Met Val Glu Asn Met Leu Asp Gln Ala Phe Lys Lys

          165   170   175

Leu Asn Pro His Glu His Pro Val Leu His Ser Asp Gln Gly Trp Gln

          180   185   190

Tyr Arg Met Arg Arg Tyr Gln Asn Ile Leu Lys Glu His Gly Ile Lys

          195   200   205

Gln Ser Met Ser Arg Lys Gly Asn Cys Leu Asp Asn Ala Val Val Glu

          210   215   220

Cys Phe Phe Gly Thr Leu Lys Ser Glu Cys Phe Tyr Leu Asp Glu Phe

225   230   235   240

Ser Asn Ile Ser Glu Leu Lys Asp Ala Val Thr Glu Tyr Ile Glu Tyr
            245   250   255

Tyr Asn Ser Arg Arg Ile Ser Leu Lys Leu Lys Gly Leu Thr Pro Ile
            260   265   270

Glu Tyr Arg Asn Gln Thr Tyr Met Pro Arg Val
          275   280

        <210> 311
        <211> 39
        <212> PRT
        <213> E. Coli

        <400> 311
Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
1   5   10   15
Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
            20   25   30
His Lys Gln Arg Gln Gly
          35

        <210> 312
        <211> 441
        <212> PRT
        <213> E. Coli

        <400> 312
Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
1   5   10   15
Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
            20   25   30
Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
          35   40   45
Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe
      50   55   60
Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu
65   70   75   80
Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr
            85   90   95
Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly
          100   105   110
Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala
          115   120   125
Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly
      130   135   140
Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala
145   150   155   160
Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu
            165   170   175
Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe
          180   185   190
Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu
          195   200   205
Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Leu Val Ala
      210   215   220
Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly
225   230   235   240

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Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg
245   250   255

Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala
260   265   270

Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala
275   280   285

Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
290   295   300

Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
305   310   315   320

Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
325   330   335

Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
340   345   350

Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
355   360   365

Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
370   375   380

Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
385   390   395   400

Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
405   410   415

Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
420   425   430

Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg
435   440

<210> 13
<211> 144
<212> PRT
<213> E. Coli

<400> 13
Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly
1   5   11   15

Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly
                        20   30

Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg
35   40   45

Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe
50   55   60

Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser
65   70   75   80

Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys
                        85   90   95

Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu
                        100   105   110

Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr
                        115   120   125

Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu
130   135   140

<210> 14
<211> 59

<212> PRT
<213> E. Coli

<400> 314

Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg
1   5   10   15

Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile
            20   25   30

Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile
        35   40   45

Asn Ala Val Ser Phe Met Val Lys Val Glu Glu
    50   55

<210> 315
<211> 167
<212> PRT
<213> E. Coli

<400> 315

Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
1   5   10   15

Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
            20   25   30

Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
        35   40   45

Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
    50   55   60

Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
65   70   75   80

Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
            85   90   95

Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
            100   105   110

Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
            115   120   125

Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
    130   135   140

Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
145   150   155   160

Val Glu Glu Ile Leu Gly Lys
                165

<210> 316
<211> 117
<212> PRT
<213> E. Coli

<400> 316

Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
1   5   10   15

Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
            20   25   30

Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
        35   40   45

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Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
    50   55   60
Thr Gly Asn Lys Asp Ala Ala Ala Ala Val Gly Lys Ala Val Ala Glu
65   70   75   80
Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
            85   90   95
Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu
            100   105   110
Ala Gly Leu Gln Phe
            115

        <210> 317
        <211> 177
        <212> PRT
        <21 > E. Coli

        <400> 317
Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
1   5   10   15
Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
            20   25   30
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
        30   40   45
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
    50   55   60
Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
65   70   75   80
Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
            85   90   95
Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
            100   115   111
Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
        115   121   1 5
Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val
        130   135   140
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
145   150   155   160
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
            165   170   175
Lys

        <210> 318
        <211> 150
        <212> PRT
        <21 > E. Coli

        <400> 318
Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn
1   5   10   15
Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu
            20   25   30
Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp
        35   40   45
Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys

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      50                    55                      60
Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
65                    70                    75                      80
Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
                      85                    90                    95
Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
                      100                   105                   110
Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
                      115                   120                   125
Val Ala
13.


        <210> 311
        <211> 131
        <211> PRT
        <213> E. Coli

        <400> 311
Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
1                     5                     10                    1
Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
                      2                     25                    30
Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
            3                     40                    45
Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
      50                    55                    60
Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
                      70                    75                    81
Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
                      85                    90                    95
Lys Lys Ala Ser Trp
                      100


        <210> 312
        <211> 175
        <211> PRT
        <213> E. Coli

        <400> 312
Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
1                     5                     10                    1
Met Thr Gln Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu
            2                     25                    30
Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys
            3                     40                    45
Leu Leu Arg Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys
      50                    55                    60
Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
6                     70                    75                    8
Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met
                      85                    90                    95
Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg
                      100                   105                   110
Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr
```

<210> 323
<211> 188
<21.> PRT
<213> E. Coli

<400> 323

```
Met Phe Lys Gly Gln Lys Thr Leu Ala Ala Leu Ala Val Ser Leu Leu
1               5                   10                  15
Phe Thr Ala Pro Val Tyr Ala Ala Asp Glu Gly Ser Gly Glu Ile His
                20                  25                  30
Phe Lys Gly Glu Val Ile Glu Ala Pro Cys Glu Ile His Pro Glu Asp
            35                  40                  45
Ile Asp Lys Asn Ile Asp Leu Gly Gln Val Thr Thr Thr His Ile Asn
        50                  55                  60
Arg Glu His His Ser Asn Lys Val Ala Val Asp Ile Arg Leu Ile Asn
65                  70                  75                  80
Cys Asp Leu Pro Ala Ser Asp Asn Gly Ser Gly Met Pro Val Ser Lys
                85                  90                  95
Val Gly Val Thr Phe Asp Ser Thr Ala Lys Thr Thr Gly Ala Thr Pro
                100                 105                 110
Leu Leu Ser Asn Thr Ser Ala Gly Glu Ala Thr Gly Val Gly Val Arg
            115                 120                 125
Leu Met Asp Lys Asn Asp Gly Asn Ile Val Leu Gly Ser Ala Ala Pro
        130                 135                 140
Asp Leu Asp Leu Asp Ala Ser Ser Ser Glu Gln Thr Leu Asn Phe Phe
145                 150                 155                 160
Ala Trp Met Gly Gln Ile Asp Asn Ala Val Asp Val Thr Ala Gly Glu
                165                 170                 175
Val Thr Ala Asn Ala Thr Tyr Val Leu Asp Tyr Lys
                180                 185
```

<210> 114
<211> 417
<21.> PRT
<213> E. Coli

<400> 114

```
Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val
1               5                   10                  15
Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile
                20                  25                  30
Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr
            35                  40                  45
Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu
        50                  55                  60
Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp
65                  70                  75                  80
Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro
                85                  90                  95
Thr Gln Glu Gln Tyr Asp Glu Phe Lys Thr Thr Val Thr Arg His Thr
                100                 105                 110
Met Ile His Glu Gln Ile Thr Arg Leu Phe His Ala Phe Arg Arg Asp
            115                 120                 125
Ser His Pro Met Ala Val Met Cys Gly Ile Thr Gly Ala Leu Ala Ala
        130                 135                 140
Phe Tyr His Asp Ser Leu Asp Val Asn Asn Pro Arg His Arg Glu Ile
```

```
145                    150                      155                      160
Ala Ala Phe Arg Leu Leu Ser Lys Met Pro Thr Met Ala Ala Met Cys
                165
Tyr Lys Tyr Ser Ile Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu
                          170                      175
Ser Tyr Ala Gly Asn Phe Leu Asn Met Met Phe Ser Thr Pro Cys Glu
                180                      185                      190
Pro Tyr Glu Val Asn Pro Ile Leu Glu Arg Ala Met Asp Arg Ile Leu
          195                      200                      205
Ile Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg
          210                      215                      220
Thr Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly
          225                      230                      235      240
Ile Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Ala
                245                      250                      255
Leu Lys Met Leu Glu Glu Ile Ser Ser Val Lys His Ile Pro Glu Phe
                260                      265                      270
Val Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe
                275                      280                      285
Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg
     290                      295                      300
Glu Thr Lys His Glu Val Leu Lys Glu Leu Gly Thr Lys Asp Asp Leu
305                      310                      315            320
Leu Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr
     325                      330                      335
Phe Ile Glu Lys Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile
          340                      345                      350
Ile Leu Lys Ala Met Gly Ile Pro Ser Ser Met Phe Thr Val Ile Phe
     355                      360                      365
Ala Met Ala Arg Thr Val Gly Trp Ile Ala His Trp Ser Glu Met His
     370                      375                      380
Ser Asp Gly Met Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr
385                      390                      395            400
Glu Lys Arg Asp Phe Lys Ser Asp Ile Lys Arg
          405                      410            415
                420            425
```

```
<210> 3.6
<211> 377
<212> PRT
<213> E. Coli

<400> 3.6
```

```
Met Lys Val Thr Leu Pro Glu Phe Glu Arg Ala Gly Val Met Val Val
 1                                      10                15
Gly Asp Val Met Leu Asp Arg Tyr Trp Tyr Gly Arg Thr Ser Arg Ile
          20                      25                      30
Ser Pro Glu Ala Pro Val Pro Val Val Lys Val Asn Thr Ile Glu Glu
          35                      40                      45
Arg Pro Gly Gly Ala Ala Asn Val Ala Met Asn Ile Ala Ser Leu Gly
          50                      55                      60
Ala Asn Ala Arg Leu Val Gly Leu Thr Gly Ile Asp Asp Ala Ala Arg
65                      70                      75            80
Ala Leu Ser Lys Ser Leu Ala Asp Val Asn Val Lys Cys Asp Phe Val
                85                      90                      95
Ser Val Pro Thr His Pro Thr Ile Thr Lys Leu Arg Val Leu Ser Arg
          100                      105                      110
```

Asn Gln Gln Leu Ile Arg Leu Asp Phe Glu Glu Gly Phe Glu Gly Val
          115   120   125

Asp Pro Gln Pro Leu His Glu Arg Ile Asn Gln Ala Leu Ser Ser Ile
          130   135   140

Gly Ala Leu Val Leu Ser Asp Tyr Ala Lys Gly Ala Leu Ala Ser Val
     145   150   155   160

Gln Gln Met Ile Gln Leu Ala Arg Lys Ala Gly Val Pro Val Leu Ile
               165   170   175

Asp Pro Lys Gly Thr Asp Phe Glu Arg Tyr Arg Gly Ala Thr Leu Leu
          180   185   190

Thr Pro Asn Leu Ser Glu Phe Glu Ala Val Val Gly Lys Cys Lys Thr
          195   200   205

Glu Glu Glu Ile Val Glu Arg Gly Met Lys Leu Ile Ala Asp Tyr Glu
          210   215   220

Leu Ser Ala Leu Leu Val Thr Arg Ser Glu Gln Gly Met Ser Leu Leu
     225   230   235   240

Gln Pro Gly Lys Ala Pro Leu His Met Pro Thr Gln Ala Gln Glu Val
               245   250   255

Tyr Asp Val Thr Gly Ala Gly Asp Thr Val Ile Gly Val Leu Ala Ala
          260   265   270

Thr Leu Ala Ala Gly Asn Ser Leu Glu Glu Ala Cys Phe Phe Ala Asn
          275   280   285

Ala Ala Ala Gly Val Val Val Gly Lys Leu Gly Thr Ser Thr Val Ser
     291   295   300

Pro Ile Glu Leu Glu Asn Ala Val Arg Gly Arg Ala Asp Thr Gly Phe
305   310   315   320

Gly Val Met Thr Glu Glu Glu Leu Lys Leu Ala Val Ala Ala Ala Arg
          325   330   335

Lys Arg Gly Glu Lys Val Val Met Thr Asn Gly Val Phe Asp Ile Leu
          340   345   350

His Ala Gly His Val Ser Tyr Leu Ala Asn Ala Arg Lys Leu Gly Asp
          355   360   365

Arg Leu Ile Val Ala Val Asn Ser Asp Ala Ser Thr Lys Arg Leu Lys
          370   375   380

Gly Asp Ser Arg Pro Val Asn Pro Leu Glu Gln Arg Met Ile Val Leu
385   390   395   400

Gly Ala Leu Glu Ala Val Asp Trp Val Val Ser Phe Glu Glu Asp Thr
               405   410   415

Pro Gln Arg Leu Ile Ala Gly Ile Leu Pro Asp Leu Leu Val Lys Gly
               420   425   430

Gly Asp Tyr Lys Pro Glu Glu Ile Ala Gly Ser Lys Glu Val Trp Ala
          435   440   445

Asn Gly Gly Glu Val Leu Val Leu Asn Phe Glu Asp Gly Cys Ser Thr
          450   455   460

Thr Asn Ile Ile Lys Lys Ile Gln Gln Asp Lys Lys Gly
465   470   475

     <210> 5 6
     <211> 936
     <212> PRT
     <213> E. Coli

     <400> 5 6

Met Lys Pro Leu Ser Ser Pro Leu Gln Gln Tyr Trp Gln Thr Val Val
1   5   10   15

Glu Arg Leu Pro Glu Pro Leu Ala Glu Glu Ser Leu Ser Ala Gln Ala

```
            20                  25                  30
Lys Ser Val Leu Thr Phe Ser Asp Phe Val Gln Asp Ser Val Ile Ala
        35                  40                  45
His Pro Glu Trp Leu Thr Glu Leu Glu Ser Gln Pro Pro Gln Ala Asp
    50                  55                  60
Glu Trp Gln His Tyr Ala Ala Trp Leu Gln Glu Ala Leu Lys Asn Val
65                  70                  75                  80
Ser Asp Glu Ala Gly Leu Met Arg Glu Leu Arg Leu Phe Arg Arg Arg
                    85                  90                  95
Ile Met Val Arg Ile Ala Trp Ala Gln Thr Leu Ala Leu Val Thr Glu
                100                 105                 110
Glu Ser Ile Leu Gln Gln Leu Ser Tyr Leu Ala Glu Thr Leu Ile Val
                115                 120                 125
Ala Ala Arg Asp Trp Leu Tyr Asp Ala Lys Cys Arg Glu Trp Gly Thr
            130                 135                 140
Pro Gly Asn Ala Gln Gly Glu Ala Gln Pro Leu Leu Ile Leu Gly Met
    145                 150                 155                 160
Gly Lys Leu Gly Gly Gly Glu Leu Asn Phe Ser Ser Asp Ile Asp Leu
                165                 170                 175
Ile Phe Ala Trp Pro Glu His Gly Cys Thr Gln Gly Gly Arg Arg Glu
                180                 185                 190
Leu Asp Asn Ala Gln Phe Phe Thr Arg Met Gly Gln Arg Leu Ile Lys
            195                 200                 205
Val Leu Asp Gln Pro Thr Gln Asp Gly Phe Val Tyr Arg Val Asp Met
    210                 215                 220
Arg Leu Arg Pro Phe Gly Glu Ser Gly Pro Leu Val Leu Ser Phe Ala
225                 230                 235                 240
Ala Leu Glu Arg Tyr Tyr Gln Glu Gln Gly Arg Asp Trp Glu Arg Tyr
                245                 250                 255
Ala Met Val Lys Ala Arg Ile Met Gly Asp Ser Glu Gly Val Tyr Ala
            260                 265                 270
Asn Glu Leu Arg Ala Met Leu Arg Pro Phe Val Phe Arg Arg Tyr Ile
    275                 280                 285
Asp Phe Ser Val Ile Gln Ser Leu Arg Asn Met Lys Gly Met Ile Ala
290                 295                 300
Arg Glu Val Arg Arg Arg Gly Leu Thr Asp Asn Ile Lys Leu Gly Ala
305                 310                 315                 320
Gly Gly Ile Arg Glu Ile Glu Phe Ile Val Gln Val Phe Gln Leu Ile
                325                 330                 335
Arg Gly Gly Arg Glu Pro Ser Leu Gln Ser Arg Ser Leu Leu Pro Thr
    340                 345                 350
Leu Ser Ala Ile Ala Glu Leu His Leu Leu Ser Gln Asn Asp Ala Glu
            355                 360                 365
Gln Leu Arg Val Ala Tyr Leu Phe Leu Arg Arg Leu Glu Asn Leu Leu
    370                 375                 380
Gln Ser Ile Asn Asp Glu Gln Thr Gln Thr Leu Pro Ser Asp Glu Leu
385                 390                 395                 400
Asn Arg Ala Arg Leu Ala Trp Ala Met Asp Phe Ala Asp Trp Pro Gln
                405                 410                 415
Leu Thr Gly Ala Leu Thr Ala His Met Thr Asn Val Arg Arg Val Phe
            420                 425                 430
Asn Gln Leu Ile Gly Asp Asp Glu Ser Glu Thr Gln Glu Glu Ser Leu
    435                 440                 445
Ser Glu Gln Trp Arg Glu Leu Trp Gln Asp Ala Leu Gln Glu Asp Asp
    450                 455                 460
Thr Thr Pro Val Leu Ala His Leu Ser Glu Asp Asp Arg Lys Gln Val
465                 470                 475                 480
```

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Leu Thr Leu Ile Ala Asp Phe Arg Lys Glu Leu Asp Lys Arg Thr Ile
                    485   440   445
Gly Pro Arg Gly Arg Gln Val Leu Asp His Leu Met Pro His Leu Leu
                500   505   510
Ser Asp Val Cys Ala Arg Glu Asp Ala Ala Val Thr Leu Ser Arg Ile
            515   520   525
Thr Ala Leu Leu Val Gly Ile Val Thr Arg Thr Thr Tyr Leu Glu Leu
        530   535   540
Leu Ser Glu Phe Pro Ala Ala Leu Lys His Leu Ile Ser Leu Cys Ala
545   550   555   560
Ala Ser Pro Met Ile Ala Ser Gln Leu Ala Arg Tyr Pro Leu Leu Leu
                565   570   575
Asp Glu Leu Leu Asp Pro Asn Thr Leu Tyr Gln Pro Thr Ala Thr Asp
                580   585   590
Ala Tyr Arg Asp Glu Leu Arg Gln Tyr Leu Leu Arg Val Pro Glu Asp
            595   600   605
Asp Glu Glu Gln Gln Leu Glu Ala Leu Arg Gln Phe Lys Gln Ala Gln
        610   615   620
Leu Leu Arg Ile Ala Ala Ala Asp Ile Ala Gly Thr Leu Pro Val Met
625   630   635   640
Lys Val Ser Asp His Leu Thr Trp Leu Ala Glu Ala Met Ile Asp Ala
                645   650   655
Val Val Gln Gln Ala Trp Val Gln Met Val Ala Arg Tyr Gly Lys Pro
                660   665   670
Asn His Leu Asn Glu Arg Glu Gly Arg Gly Phe Ala Val Val Gly Tyr
            675   680   685
Gly Lys Leu Trp Gly Trp Glu Leu Gly Tyr Ser Ser Asp Leu Asp Leu
        690   695   700
Ile Phe Leu His Asp Tyr Pro Met Asp Ala Met Thr Asp Gly Glu Arg
705   710   715   720
Glu Ile Asp Gly Arg Gln Phe Tyr Leu Arg Leu Ala Gln Arg Ile Met
                725   730   735
His Leu Phe Ser Thr Arg Thr Ser Ser Gly Ile Leu Tyr Glu Val Asp
                740   745   750
Ala Arg Leu Arg Pro Ser Gly Ala Ala Gly Met Leu Val Thr Ser Ala
            755   760   765
Glu Ala Phe Ala Asp Tyr Gln Lys Asn Glu Ala Trp Thr Trp Glu His
        770   775   780
Gln Ala Leu Val Arg Ala Arg Val Val Tyr Gly Asp Pro Gln Leu Thr
785   790   795   800
Ala His Phe Asp Ala Val Arg Arg Glu Ile Met Thr Leu Pro Arg Glu
                805   810   815
Gly Lys Thr Leu Gln Thr Glu Val Arg Glu Met Arg Glu Lys Met Arg
                820   825   830
Ala His Leu Gly Asn Lys His Arg Asp Arg Phe Asp Ile Lys Ala Asp
            835   840   845
Glu Gly Gly Leu Thr Asp Ile Glu Phe Ile Thr Gln Tyr Leu Val Leu
        850   855   860
Arg Tyr Ala His Glu Lys Pro Lys Leu Thr Arg Trp Ser Asp Asn Val
865   870   875   880
Arg Ile Leu Glu Leu Leu Ala Gln Asn Asp Ile Met Glu Gln Gln Glu
                885   890   895
Ala Met Ala Leu Thr Arg Ala Tyr Thr Thr Leu Arg Asp Glu Leu His
            900   905   910
His Leu Ala Leu Gln Glu Leu Pro Gly His Val Ser Glu Asp Cys Phe
        915   920   925
Thr Ala Glu Arg Glu Leu Val Arg Ala Ser Trp Gln Lys Trp Leu Val

```
        930               935               940
Glu Glu
945
```

```
<210> 327
<211> 443
<212> PRT
<213> E. Coli

<400> 27
```

```
Met Ala Gln Glu Ile Glu Leu Lys Phe Ile Val Asn His Ser Ala Val
1               5               10              15

Glu Ala Leu Arg Asp His Leu Asn Thr Leu Gly Gly Glu His His Asp
                20              25              30

Pro Val Gln Leu Leu Asn Ile Tyr Tyr Glu Thr Pro Asp Asn Trp Leu
        35              40              45

Arg Gly His Asp Met Gly Leu Arg Ile Arg Gly Glu Asn Gly Arg Tyr
        50              55              60

Glu Met Thr Met Lys Val Ala Gly Arg Val Thr Gly Gly Leu His Gln
65              70              75              80

Arg Pro Glu Tyr Asn Val Ala Leu Ser Glu Pro Thr Leu Asp Leu Ala
                    85              90              95

Gln Leu Pro Thr Glu Val Trp Pro Asn Gly Glu Leu Pro Ala Asp Leu
        100             105             110

Ala Ser Arg Val Gln Pro Leu Phe Ser Thr Asp Phe Tyr Arg Glu Lys
        115             120             125

Trp Leu Val Ala Val Asp Gly Ser Gln Ile Glu Ile Ala Leu Asp Gln
        130             135             140

Gly Glu Val Lys Ala Gly Glu Phe Ala Glu Pro Ile Cys Glu Leu Glu
145             150             155             160

Leu Glu Leu Leu Ser Gly Asp Thr Arg Ala Val Leu Lys Leu Ala Asn
                    165             170             175

Gln Leu Val Ser Gln Thr Gly Leu Arg Gln Gly Ser Leu Ser Lys Ala
                    180             185             190

Ala Arg Gly Tyr His Leu Ala Gln Gly Asn Pro Ala Arg Glu Ile Lys
                195             200             205

Pro Thr Thr Ile Leu His Val Ala Ala Lys Ala Asp Val Glu Gln Gly
        210             215             220

Leu Glu Ala Ala Leu Glu Leu Ala Leu Ala Gln Trp Gln Tyr His Glu
225             230             235             240

Glu Leu Trp Val Arg Gly Asn Asp Ala Ala Lys Glu Gln Val Leu Ala
                245             250             255

Ala Ile Ser Leu Val Arg His Thr Leu Met Leu Phe Gly Gly Ile Val
        260             265             270

Pro Arg Lys Ala Ser Thr His Leu Arg Asp Leu Leu Thr Gln Cys Glu
        275             280             285

Ala Thr Ile Ala Ser Ala Val Ser Ala Val Thr Ala Val Tyr Ser Thr
        290             295             300

Glu Thr Ala Met Ala Lys Leu Ala Leu Thr Gln Trp Leu Val Ser Lys
305             310             315             320

Ala Trp Gln Pro Phe Leu Asp Ala Lys Ala Gln Gly Lys Ile Ser Asp
                325             330             335

Ser Phe Lys Arg Phe Ala Asp Ile His Leu Ser Arg His Ala Ala Glu
                340             345             350

Leu Lys Ser Val Phe Cys Gln Pro Leu Gly Asp Arg Tyr Arg Asp Gln
```

```
              355                    360                    365
Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Leu Ala Gly
         370              375              380
Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly
385              390              395              400
Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe
                   405              410              415
Arg Asn Gln Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys
              420              425              430
Arg
```

```
    <210> 318
    <211> 70
    <212> PRT
    <213> E. Coli

    <400> 318
Met Ser Gly Lys Met Thr Gly Ile Val Lys Trp Phe Asn Ala Asp Lys
1                5                10               15
Gly Phe Gly Phe Ile Thr Pro Asp Asp Gly Ser Lys Asp Val Phe Val
                20               25               30
His Phe Ser Ala Ile Gln Asn Asp Gly Tyr Lys Ser Leu Asp Glu Gly
                35               40               45
Gln Lys Val Ser Phe Thr Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
         50               55               60
Gly Asn Val Thr Ser Leu
65               70
```

```
    <210> 319
    <211> 143
    <212> PRT
    <213> E. Coli

    <400> 319
Met Arg Asp Ile Val Asp Pro Val Phe Ser Ile Gly Ile Ser Ser Leu
1                5                10               15
Trp Asp Glu Leu Arg His Met Pro Ala Gly Gly Val Trp Trp Phe Asn
              20               25               30
Val Asp Arg His Glu Asp Ala Ile Ser Leu Ala Asn Gln Thr Ile Ala
         35               40               45
Ser Gln Ala Glu Thr Ala His Val Ala Val Ile Ser Met Asp Ser Asp
         50               55               60
Pro Ala Lys Ile Phe Gln Leu Asp Asp Ser Gln Gly Pro Glu Lys Ile
65               70               75               80
Lys Leu Phe Ser Met Leu Asn His Glu Lys Gly Leu Tyr Tyr Leu Thr
                  85               90               95
Arg Asp Leu Gln Cys Ser Ile Asp Pro His Asn Tyr Leu Phe Ile Leu
                  100              105              110
Val Cys Ala Asn Asn Ala Trp Gln Asn Ile Pro Ala Glu Arg Leu Arg
              115              120              125
Ser Trp Leu Asp Lys Met Asn Lys Trp Ser Arg Leu Asn His Cys Ser
         130              135              140
```

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Leu Leu Val Ile Asn Pro Gly Asn Asn Asn Asp Lys Gln Phe Ser Leu
145   150   155   160

Leu Leu Glu Glu Tyr Arg Ser Leu Phe Gly Leu Ala Ser Leu Arg Phe
165   170   175

Gln Gly Asp Gln His Leu Leu Asp Ile Ala Phe Trp Cys Asn Glu Lys
180   185   190

Gly Val Ser Ala Arg Gln Gln Leu Ser Val Gln Gln Gln Asn Gly Ile
195   200   205

Trp Thr Leu Val Gln Ser Glu Glu Ala Glu Ile Gln Pro Arg Ser Asp
210   215   220

Glu Lys Arg Ile Leu Ser Asn Val Ala Val Leu Glu Gly Ala Pro Pro
225   230   235   241

Leu Ser Glu His Trp Gln Leu Phe Asn Asn Asn Glu Val Leu Phe Asn
245   251   255

Glu Ala Arg Thr Ala Gln Ala Ala Thr Val Val Phe Ser Leu Gln Gln
260   265   270

Asn Ala Gln Ile Glu Pro Leu Ala Arg Ser Ile His Thr Leu Arg Arg
275   280   285

Gln Arg Gly Ser Ala Met Lys Ile Leu Val Arg Glu Asn Thr Ala Ser
290   295   300

Leu Arg Ala Thr Asp Glu Arg Leu Leu Leu Ala Cys Gly Ala Asn Met
305   310   315   320

Val Ile Pro Trp Asn Ala Pro Leu Ser Arg Cys Leu Thr Met Ile Glu
325   330   335

Ser Val Gln Gly Gln Lys Phe Ser Arg Tyr Val Pro Glu Asp Ile Thr
340   345   350

Thr Leu Leu Ser Met Thr Gln Pro Leu Lys Leu Arg Gly Phe Gln Lys
355   360   365

Trp Asp Val Phe Cys Asn Ala Val Asn Asn Met Met Asn Asn Pro Leu
370   375   380

Leu Pro Ala His Gly Lys Gly Val Leu Val Ala Leu Arg Pro Val Pro
385   390   395   400

Gly Ile Arg Val Glu Gln Ala Leu Thr Leu Cys Arg Pro Asn Arg Thr
405   410   415

Gly Asp Ile Met Thr Ile Gly Gly Asn Arg Leu Val Leu Phe Leu Ser
420   425   430

Phe Cys Arg Ile Asn Asp Leu Asp Thr Ala Leu Asn His Ile Phe Pro
435   440   445

Leu Pro Thr Gly Asp Ile Phe Ser Asn Arg Met Val Trp Phe Glu Asp
451   455   460

Asp Gln Ile Ser Ala Glu Leu Val Gln Met Arg Leu Leu Ala Pro Glu
465   470   475   480

Gln Trp Gly Met Pro Leu Pro Leu Thr Gln Ser Ser Lys Pro Val Ile
485   490   495

Asn Ala Glu His Asp Gly Arg His Trp Arg Arg Ile Pro Glu Pro Met
500   505   510

Arg Leu Leu Asp Asp Ala Val Glu Arg Ser Ser
511   520

<210> 330
<211> 53
<212> PRT
<213> E. Coli

<400> 330
Met Thr Ile Ser Asp Ile Ile Glu Ile Ile Val Val Cys Ala Leu Ile

```
 1           5                10                 15
Phe Phe Pro Leu Gly Tyr Leu Ala Arg His Ser Leu Arg Arg Ile Arg
             20                    25                30
Asp Thr Leu Arg Leu Phe Phe Ala Lys Pro Arg Tyr Val Lys Pro Ala
             35                    40                45
Gly Thr Leu Arg Arg Thr Glu Lys Ala Arg Ala Thr Lys Lys
        50                    55                60


    <210> 331
    <211> 339
    <212> PRT
    <213> E. Coli


    <400> 331

Met Thr Gln Phe Thr Gln Asn Thr Ala Met Pro Ser Ser Leu Trp Gln
1            5                10                 15
Tyr Trp Arg Gly Leu Ser Gly Trp Asn Phe Tyr Phe Leu Val Lys Phe
             20                25                30
Gly Leu Leu Trp Ala Gly Tyr Leu Asn Phe His Pro Leu Leu Asn Leu
             35                40                45
Val Pro Ala Ala Phe Leu Leu Met Pro Leu Pro Arg Tyr Ser Leu His
        50                55                60
Arg Leu Arg His Trp Ile Ala Leu Pro Ile Gly Phe Ala Leu Phe Trp
65           70                75                80
His Asp Thr Trp Leu Pro Gly Pro Glu Ser Ile Met Ser Gln Gly Ser
             85                90                95
Gln Val Ala Gly Phe Ser Thr Asp Tyr Leu Ile Asp Leu Val Thr Arg
             100               105               110
Phe Ile Asn Trp Gln Met Ile Gly Ala Ile Phe Val Leu Leu Val Ala
             115               120               125
Trp Leu Phe Leu Ser Gln Trp Ile Arg Ile Thr Val Phe Val Val Ala
             135               140
Ile Leu Leu Trp Leu Asn Val Leu Thr Leu Ala Gly Pro Ser Phe Ser
145               150               155               160
Leu Trp Pro Ala Gly Gln Pro Thr Thr Thr Val Thr Thr Thr Gly Gly
             165               170               175
Asn Ala Ala Ala Thr Val Ala Ala Thr Gly Gly Ala Pro Val Val Gly
             181               185               190
Asp Met Pro Ala Gln Thr Ala Pro Pro Thr Thr Ala Asn Leu Asn Ala
             19?               200               205
Trp Leu Asn Asn Phe Tyr Asn Ala Glu Ala Lys Arg Lys Ser Thr Phe
             210               215               220
Pro Ser Ser Leu Pro Ala Asp Ala Gln Pro Phe Glu Leu Leu Val Ile
125               230               235               240
Asn Ile Cys Ser Leu Ser Trp Ser Asp Ile Glu Ala Ala Gly Leu Met
             245               250               255
Ser His Pro Leu Trp Ser His Phe Asp Ile Glu Phe Lys Asn Phe Asn
             260               265               270
Ser Ala Thr Ser Tyr Ser Gly Pro Ala Ala Ile Arg Leu Leu Arg Ala
             275               280               285
Ser Cys Gly Gln Thr Ser His Thr Asn Leu Tyr Gln Pro Ala Asn Asn
             290               295               300
Asp Cys Tyr Leu Phe Asp Asn Leu Ser Lys Leu Gly Phe Thr Gln His
305               310               315               320
Leu Met Met Gly His Asn Gly Gln Phe Gly Gly Phe Leu Lys Glu Val
             325               330               335
```

Arg Glu Asn Gly Gly Met Gln Ser Glu Leu Met Asp Gln Thr Asn Leu
          340   345   350
Pro Val Ile Leu Leu Gly Phe Asp Gly Ser Pro Val Tyr Asp Asp Thr
          355   360   365
Ala Val Leu Asn Arg Trp Leu Asp Val Thr Glu Lys Asp Lys Asn Ser
          370   375   380
Arg Ser Ala Thr Phe Tyr Asn Thr Leu Pro Leu His Asp Gly Asn His
335   390   395   400
Tyr Pro Gly Val Ser Lys Thr Ala Asp Tyr Lys Ala Arg Ala Gln Lys
             405   410   415
Phe Phe Asp Glu Leu Asp Ala Phe Phe Thr Glu Leu Glu Lys Ser Gly
             420   4?5   430
Arg Lys Val Met Val Val Val Val Pro Glu His Gly Gly Ala Leu Lys
          4?5   440   445
Gly Asp Arg Met Gln Val Ser Gly Leu Arg Asp Ile Pro Ser Pro Ser
          450   455   460
Ile Thr Asp Val Pro Val Gly Val Lys Phe Phe Gly Met Lys Ala Pro
465   470   475   480
His Gln Gly Ala Pro Ile Val Ile Glu Gln Pro Ser Ser Phe Leu Ala
             485   490   495
Ile Ser Asp Leu Val Val Arg Val Leu Asp Gly Lys Ile Phe Thr Glu
          500   505   510
Asp Asn Val Asp Trp Lys Lys Leu Thr Ser Gly Leu Pro Gln Thr Ala
          515   520   525
Pro Val Ser Glu Asn Ser Asn Ala Val Val Ile Gln Tyr Gln Asp Lys
          530   535   540
Pro Tyr Val Arg Leu Asn Gly Gly Asp Trp Val Pro Tyr Pro Gln
545   550   555

<210> ?1
<211> 127
<21?> PRT
<213> E. Coli

<400> ?

Met Glu Gly Ser Arg Met Lys Tyr Arg Ile Ala Leu Ala Val Ser Leu
1   5   10   15
Phe Ala Leu Ser Ala Gly Ser Tyr Ala Thr Thr Leu Cys Gln Glu Lys
          20   25   30
Gln Gln Asn Ile Leu Lys Glu Ile Ser Tyr Ala Glu Lys His Gln Asn
          35   40   45
Gln Asn Arg Ile Asp Gly Leu Asn Lys Ala Leu Ser Glu Val Arg Ala
          50   55   60
Asn Tyr Ser Asp Ser Gln Leu Arg Ala Asp His Gln Lys Lys Ile Ala
65   70   75   80
Lys Gln Lys Asp Glu Val Ala Glu Arg Gln Gln Asp Leu Ala Glu Ala
             85   90   95
Lys Gln Lys Gly Asp Ala Asp Lys Ile Ala Lys Arg Glu Arg Lys Leu
          100   105   110
Ala Glu Ala Gln Glu Glu Leu Lys Lys Leu Glu Ala Arg Asp Tyr
          115   120   125

<210> ??
<211> 1?1
<212> PRT

<213> E. Coli

<400> 333

Met	Ser	Lys	Glu	His	Thr	Thr	Glu	His	Leu	Arg	Ala	Glu	Leu	Lys	Ser
1				5					10					15	
Leu	Ser	Asp	Thr	Leu	Glu	Glu	Val	Leu	Ser	Ser	Ser	Gly	Glu	Lys	Ser
			20					25					30		
Lys	Glu	Gln	Leu	Ser	Lys	Ile	Arg	Ser	Lys	Ala	Glu	Gln	Ala	Leu	Lys
			35					40					45		
Gln	Ser	Arg	Tyr	Arg	Leu	Gly	Glu	Thr	Gly	Asp	Ala	Ile	Ala	Lys	Gln
			50					55					60		
Thr	Arg	Val	Ala	Ala	Ala	Arg	Ala	Asp	Glu	Tyr	Val	Arg	Glu	Asn	Pro
65					70					75					80
Trp	Thr	Gly	Val	Gly	Ile	Gly	Ala	Ala	Ile	Gly	Val	Val	Leu	Gly	Val
				85					90					95	
Leu	Leu	Ser	Arg	Arg											
			100												

<110> 334
<111> 104
<112> PRT
<213> E. Coli

<400> 334

Met	Ala	Asp	Thr	His	His	Ala	Gln	Gly	Pro	Gly	Lys	Ser	Val	Leu	Gly
1				5					10					15	
Ile	Gly	Gln	Arg	Ile	Val	Ser	Ile	Met	Val	Glu	Met	Val	Gln	Thr	Arg
			20					25					30		
Leu	Arg	Leu	Ala	Val	Val	Glu	Leu	Glu	Gln	Glu	Lys	Ala	Asn	Leu	Phe
			35					40					45		
Gln	Leu	Leu	Leu	Met	Leu	Gly	Leu	Thr	Met	Leu	Phe	Ala	Ala	Phe	Gly
			50					55					60		
Leu	Met	Ser	Leu	Met	Val	Leu	Ile	Ile	Trp	Ala	Val	Asp	Pro	Gln	Tyr
65					70					75					80
Arg	Leu	Asn	Ala	Met	Ile	Ala	Thr	Thr	Val	Val	Leu	Leu	Leu	Leu	Ala
				85					91					95	
Leu	Ile	Gly	Gly	Ile	Trp	Thr	Leu	Arg	Lys	Ser	Arg	Lys	Ser	Thr	Leu
			100					105					110		
Leu	Arg	His	Thr	Arg	His	Glu	Leu	Ala	Asn	Asp	Arg	Gln	Leu	Leu	Glu
			115					120					125		
Glu	Glu	Ser	Arg	Glu	Gln										
			130												

<110> 335
<111> 99
<112> PRT
<213> E. Coli

<400> 335

Met	Ser	Ser	Lys	Val	Glu	Arg	Glu	Arg	Arg	Lys	Ala	Gln	Leu	Leu	Ser
1				5					10					15	
Gln	Ile	Gln	Gln	Gln	Arg	Leu	Asp	Leu	Ser	Ala	Ser	Arg	Arg	Glu	Trp
			20					25					30		
Leu	Glu	Thr	Thr	Gly	Ala	Tyr	Asp	Arg	Arg	Trp	Asn	Met	Leu	Leu	Ser

```
                35                      40                      45
Leu Arg Ser Trp Ala Leu Val Gly Ser Ser Val Met Ala Ile Trp Thr
        50                      55                      60
Ile Arg His Pro Asn Met Leu Val Arg Trp Ala Arg Arg Gly Phe Gly
65                      70                      75                      80
Val Trp Ser Ala Trp Arg Leu Val Lys Thr Thr Leu Lys Gln Gln Gln
                        85                      90                      95
Leu Arg Gly


        <210> 136
        <211> 160
        <212> PRT
        <213> E. Coli

        <400> 136
Met Ile Leu Ser Ile Asp Ser Asn Asp Ala Asn Thr Ala Pro Leu His
1                   5                   10                      15
Lys Lys Thr Ile Ser Ser Leu Ser Gly Ala Val Glu Ser Met Met Lys
                    20                  25                      30
Lys Leu Gly Asp Val Gly Val Leu Val Ala Arg Ile Leu Met Pro Ile
            35                  40                      45
Leu Phe Ile Thr Ala Gly Trp Gly Lys Ile Thr Gly Tyr Ala Gly Thr
        50                  55                      60
Gln Gln Tyr Met Glu Ala Met Gly Val Pro Gly Phe Met Leu Pro Leu
65                  70                      75                      80
Val Ile Leu Leu Glu Phe Gly Gly Gly Leu Ala Ile Leu Phe Gly Phe
                    85                      90                      95
Leu Thr Arg Thr Thr Ala Leu Phe Thr Ala Gly Phe Thr Leu Leu Thr
                100                     105                     110
Ala Phe Leu Phe His Ser Asn Phe Ala Glu Gly Val Asn Ser Leu Met
                115                     120                     125
Phe Met Lys Asn Leu Thr Ile Ser Gly Gly Phe Leu Leu Leu Ala Ile
            130                     135                     140
Thr Gly Pro Gly Ala Tyr Ser Ile Asp Arg Leu Leu Asn Lys Lys Trp
145                     150                     155                     160


        <210> 137
        <211> 149
        <212> PRT
        <213> E. Coli

        <400> 137
Met Ile Lys Lys Thr Thr Glu Ile Asp Ala Ile Leu Leu Asn Leu Asn
1                   5                   10                      15
Lys Ala Ile Asp Ala His Tyr Gln Trp Leu Val Ser Met Phe His Ser
                    20                  25                      30
Val Val Ala Arg Asp Ala Ser Lys Pro Glu Ile Thr Asp Asn His Ser
            35                  40                      45
Tyr Gly Leu Cys Gln Phe Gly Arg Trp Ile Asp His Leu Gly Pro Leu
        50                  55                      60
Asp Asn Asp Glu Leu Pro Tyr Val Arg Leu Met Asp Ser Ala His Gln
65                  70                      75                      80
```

His Met His Asn Cys Gly Arg Glu Leu Met Leu Ala Ile Val Glu Asn
                85   90   95

His Trp Gln Asp Ala His Phe Asp Ala Phe Gln Glu Gly Leu Leu Ser
               100   105   110

Phe Thr Ala Ala Leu Thr Asp Tyr Lys Ile Tyr Leu Leu Thr Ile Arg
               115   120   125

Ser Asn Met Asp Val Leu Thr Gly Leu Pro Gly Arg Arg Val Leu Asp
       130   135   140

Glu Ser Phe Asp His Gln Leu Arg Asn Ala Glu Pro Leu Asn Leu Tyr
145   150   155   160

Leu Met Leu Leu Asp Ile Asp Arg Phe Lys Leu Val Asn Asp Thr Tyr
               165   170   175

Gly His Leu Ile Gly Asp Val Val Leu Arg Thr Leu Ala Thr Tyr Leu
               180   185   190

Ala Ser Trp Thr Arg Asp Tyr Glu Thr Val Tyr Arg Tyr Gly Gly Glu
               195   200   205

Glu Phe Ile Ile Ile Val Lys Ala Ala Asn Asp Glu Glu Ala Cys Arg
       210   215   220

Ala Gly Val Arg Ile Cys Gln Leu Val Asp Asn His Ala Ile Thr His
225   230   235   240

Ser Glu Gly His Ile Asn Ile Thr Val Thr Ala Gly Val Ser Arg Ala
               245   250   255

Phe Pro Glu Glu Pro Leu Asp Val Val Ile Gly Arg Ala Asp Arg Ala
       260   265   270

Met Tyr Glu Gly Lys Gln Thr Gly Arg Asn Arg Cys Met Phe Ile Asp
       275   285

Glu Gln Asn Val Ile Asn Arg Val
       290   295

    <210> 55
    <211> 29?
    <212> PRT
    <213> E. Coli

    <400> 55

Met Arg Leu Arg Val Val Pro Gly Phe Ile Ser Pro Pro Pro Gly Phe
 1   5   11   15

Gly Gly Leu Gly Tyr Thr Pro Thr Ala Arg Ala Cys Val Asn Ile Ser
               20   25   30

Ile Pro Leu Gln Leu Arg Val Ile Asp Met Leu Asp Val Phe Thr Pro
               35   40   45

Leu Leu Lys Leu Phe Ala Asn Glu Pro Leu Glu Arg Leu Met Tyr Thr
 51   55   60

Ile Ile Ile Phe Gly Leu Thr Leu Trp Leu Ile Pro Lys Glu Phe Thr
65   70   75   80

Val Ala Phe Asn Ala Tyr Thr Glu Ile Pro Trp Leu Phe Gln Ile Ile
               85   90   95

Val Phe Ala Phe Ser Phe Val Val Ala Ile Ser Phe Ser Arg Leu Arg
               100   105   110

Ala His Ile Gln Lys His Tyr Ser Leu Leu Pro Glu Gln Arg Val Leu
               115   120   125

Leu Arg Leu Ser Glu Lys Glu Ile Ala Val Phe Lys Asp Phe Leu Lys
 15   135   140

Thr Gly Asn Leu Ile Ile Thr Ser Pro Cys Arg Asn Pro Val Met Lys
145   150   155   160

Lys Leu Glu Arg Lys Gly Ile Ile Gln His Gln Ser Asp Ser Ala Asn
           165   170   175

Cys Ser Tyr Tyr Leu Val Thr Glu Lys Tyr Ser His Phe Met Lys Leu
          180   185   190

Phe Trp Asn Ser Arg Ser Arg Arg Phe Asn Arg
       145   200

<210> 9
<211> 84
<212> PRT
<213> E. Coli

<400> 9
Met Leu Leu Gln Pro Ser Ala Arg Thr Ser Phe Gly Phe Lys Cys Phe
1   5   11   15

Ala Phe Gly Ile Arg His Gly Ser Glu Arg Ser Ile Leu Val Gly Glu
          20   25   30

His Ala Ala His Gln Gly Phe Val Val Ala Glu Val Asp Phe Leu His
          35   40   45

Phe Ala Asn Leu Thr Ser Cys Cys Tyr Val
       50   55

<210> 10
<211> 1426
<212> PRT
<213> E. Coli

<400> 10
Met Ser Gly Lys Pro Ala Ala Arg Gln Gly Asp Met Thr Gln Tyr Gly
1   5   10   15

Gly Pro Ile Val Gln Gly Ser Ala Gly Val Arg Ile Gly Ala Pro Thr
          20   25   30

Gly Val Ala Cys Ser Val Cys Pro Gly Gly Met Thr Ser Gly Asn Pro
          35   40   45

Val Asn Pro Leu Leu Gly Ala Lys Val Leu Pro Gly Glu Thr Asp Leu
       50   55   60

Ala Leu Pro Gly Pro Leu Pro Phe Ile Leu Ser Arg Thr Tyr Ser Ser
65   70   75   80

Tyr Arg Thr Lys Thr Pro Ala Pro Val Gly Val Phe Gly Pro Gly Trp
          85   90   95

Lys Ala Pro Ser Asp Ile Arg Leu Gln Leu Arg Asp Asp Gly Leu Ile
          100   105   110

Leu Asn Asp Asn Gly Gly Arg Ser Ile His Phe Glu Pro Leu Leu Pro
          115   120   125

Gly Glu Ala Val Tyr Ser Arg Ser Glu Ser Met Trp Leu Val Arg Gly
          130   135   140

Gly Lys Ala Ala Gln Pro Asp Gly His Thr Leu Ala Arg Leu Trp Gly
     145   150   155   160

Ala Leu Pro Pro Asp Ile Arg Leu Ser Pro His Leu Tyr Leu Ala Thr
          165   170   175

Asn Ser Ala Gln Gly Pro Trp Trp Ile Leu Gly Trp Ser Glu Arg Val
          180   185   190

Pro Gly Ala Glu Asp Val Leu Pro Ala Pro Leu Pro Pro Tyr Arg Val
          195   200   205

Leu Thr Gly Met Ala Asp Arg Phe Gly Arg Thr Leu Thr Tyr Arg Arg
210   215   220

Glu Ala Ala Gly Asp Leu Ala Gly Glu Ile Thr Gly Val Thr Asp Gly
225   230   235   240

Ala Gly Arg Glu Phe Arg Leu Val Leu Thr Thr Gln Ala Gln Arg Ala
               245   250   255

Glu Glu Ala Arg Thr Ser Ser Leu Ser Ser Ser Asp Ser Ser Arg Pro
               260   265   270

Leu Ser Ala Ser Ala Phe Pro Asp Thr Leu Pro Gly Thr Glu Tyr Gly
          275   280   285

Pro Asp Arg Gly Ile Arg Leu Ser Ala Val Trp Leu Met His Asp Pro
          290   295   300

Ala Tyr Pro Glu Ser Leu Pro Ala Ala Pro Leu Val Arg Tyr Thr Tyr
305   310   315   320

Thr Glu Ala Gly Glu Leu Leu Ala Val Tyr Asp Arg Ser Asn Thr Gln
               325   330   335

Val Arg Ala Phe Thr Tyr Asp Ala Gln His Pro Gly Arg Met Val Ala
               340   345   350

His Arg Tyr Ala Gly Arg Pro Glu Met Arg Tyr Arg Tyr Asp Asp Thr
          355   360   365

Gly Arg Val Val Glu Gln Leu Asn Pro Ala Gly Leu Ser Tyr Arg Tyr
          370   375   380

Leu Tyr Glu Gln Asp Arg Ile Thr Val Thr Asp Ser Leu Asn Arg Arg
385   390   395   400

Glu Val Leu His Thr Glu Gly Gly Ala Gly Leu Lys Arg Val Val Lys
               405   410   415

Lys His Leu Ala Asp Gly Ser Val Thr Arg Ser Gly Tyr Asp Ala Ala
          420   425   430

Gly Arg Leu Thr Ala Gln Thr Asp Ala Ala Gly Arg Arg Thr Glu Tyr
          435   440   445

Gly Leu Asn Val Val Ser Gly Asp Ile Thr Asp Ile Thr Thr Pro Asp
          450   455   460

Gly Arg Glu Thr Lys Phe Tyr Tyr Asn Asp Gly Asn Gln Leu Thr Ala
465   470   475   480

Val Val Ser Pro Asp Gly Leu Glu Ser Arg Arg Gly Tyr Asp Glu Pro
               485   490   495

Gly Arg Leu Val Ser Glu Thr Ser Arg Ser Gly Glu Thr Val Arg Tyr
          500   505   510

Arg Tyr Asp Asp Ala His Ser Glu Leu Pro Ala Thr Thr Thr Asp Ala
          515   520   525

Thr Gly Ser Thr Arg Gln Met Thr Trp Ser Arg Tyr Gly Gln Leu Leu
          530   535   540

Ala Phe Thr Asp Cys Ser Gly Tyr Gln Thr Arg Tyr Glu Tyr Asp Arg
545   550   555   560

Phe Gly Gln Met Thr Ala Val His Arg Glu Glu Gly Ile Ser Leu Tyr
               565   570   575

Arg Arg Tyr Asp Asn Arg Gly Arg Leu Thr Ser Val Lys Asp Ala Gln
          580   585   590

Gly Arg Glu Thr Arg Tyr Glu Tyr Asn Ala Ala Gly Asp Leu Thr Ala
          595   600   605

Val Ile Thr Pro Asp Gly Asn Arg Ser Glu Thr Gln Tyr Asp Ala Trp
          610   615   620

Gly Lys Ala Val Ser Thr Thr Gln Gly Gly Leu Thr Arg Ser Met Glu
625   630   635   640

Tyr Asp Ala Ala Gly Arg Val Ile Ser Leu Thr Asn Glu Asn Gly Ser
               645   650   655

His Ser Val Phe Ser Tyr Asp Ala Leu Asp Arg Leu Val Gln Gln Gly

Gly Phe Asp Gly Arg Thr Gln Arg Tyr His Tyr Asp Leu Thr Gly Lys
675 680 685

Leu Thr Gln Ser Glu Asp Glu Gly Leu Val Ile Leu Trp Tyr Tyr Asp
690 695 700

Glu Ser Asp Arg Ile Thr His Arg Thr Val Asn Gly Glu Pro Ala Glu
705 710 715 720

Gln Trp Gln Tyr Asp Gly His Gly Trp Leu Thr Asp Ile Ser His Leu
725 730 735

Ser Glu Gly His Arg Val Ala Val His Tyr Gly Tyr Asp Asp Lys Gly
740 745 750

Arg Leu Thr Gly Glu Lys Gln Thr Val Glu Asn Pro Glu Thr Gly Glu
755 760 765

Leu Leu Trp Gln His Glu Thr Lys His Ala Tyr Asn Glu Gln Gly Leu
770 775 780

Ala Asn Arg Val Thr Pro Asp Ser Leu Pro Pro Val Glu Trp Leu Thr
785 790 795 800

Tyr Gly Ser Gly Tyr Leu Ala Gly Met Lys Leu Gly Gly Thr Pro Leu
805 810 815

Val Glu Tyr Thr Arg Asp Arg Leu His Arg Glu Thr Val Arg Ser Phe
820 825 830

Gly Ser Met Ala Gly Ser Asn Ala Ala Tyr Glu Leu Thr Ser Thr Tyr
835 840 845

Thr Pro Ala Gly Gln Leu Gln Ser Gln His Leu Asn Ser Leu Val Tyr
850 855 860

Asp Arg Asp Tyr Gly Trp Ser Asp Asn Gly Asp Leu Val Arg Ile Ser
865 870 875 880

Gly Pro Arg Gln Thr Arg Glu Tyr Gly Tyr Ser Ala Thr Gly Arg Leu
885 890 895

Glu Ser Val Arg Thr Leu Ala Pro Asp Leu Asp Ile Arg Ile Pro Tyr
900 905 910

Ala Thr Asp Pro Ala Gly Asn Arg Leu Pro Asp Pro Glu Leu His Pro
915 920 925

Asp Ser Thr Leu Thr Val Trp Pro Asp Asn Arg Ile Ala Glu Asp Ala
930 935 940

His Tyr Val Tyr Arg His Asp Glu Tyr Gly Arg Leu Thr Glu Lys Thr
945 950 955 960

Asp Arg Ile Pro Ala Gly Val Ile Arg Thr Asp Asp Glu Arg Thr His
965 970 975

His Tyr His Tyr Asp Ser Gln His Arg Leu Val Phe Tyr Thr Arg Ile
980 985 990

Gln His Gly Glu Pro Leu Val Glu Ser Arg Tyr Leu Tyr Asp Pro Leu
995 1000 1005

Gly Arg Arg Met Ala Lys Arg Val Trp Arg Arg Glu Arg Asp Leu Thr
1010 1015 1020

Gly Trp Met Ser Leu Ser Arg Lys Pro Glu Val Thr Trp Tyr Gly Trp
1025 1030 1035 1040

Asp Gly Asp Arg Leu Thr Thr Val Gln Thr Asp Thr Thr Arg Ile Gln
1045 1050 1055

Thr Val Tyr Glu Pro Gly Ser Phe Thr Pro Leu Ile Arg Val Glu Thr
1060 1065 1070

Gln Asn Gly Glu Arg Glu Lys Ala Gln Arg Arg Ser Leu Ala Glu Thr
1075 1080 1085

Leu Gln Gln Glu Gly Ser Glu Asn Gly His Gly Val Val Phe Pro Ala
1090 1095 1100

Glu Leu Val Arg Leu Leu Asp Arg Leu Glu Glu Glu Ile Arg Ala Asp
1105 1110 1115 1120

Arg Val Ser Ser Glu Ser Arg Ala Trp Leu Ala Gln Cys Gly Leu Thr
            1125   1130   1135
Val Glu Gln Leu Ala Arg Gln Val Glu Pro Glu Tyr Thr Pro Ala Arg
            1140   1145   1150
Lys Ala His Leu Tyr His Cys Asp His Arg Gly Leu Pro Leu Ala Leu
            1155   1160   1165
Ile Ser Glu Asp Gly Asn Thr Ala Trp Ser Ala Glu Tyr Asp Glu Trp
            1170   1175   1180
Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Val Tyr Gln Pro Tyr
1185   1190   1195   1200
Arg Leu Pro Gly Gln Gln His Asp Glu Glu Ser Gly Leu Tyr Tyr Asn
            1205   1210   1215
Arg His Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr Ile Thr Gln Asp
            1220   1225   1230
Pro Met Gly Leu Lys Gly Gly Trp Asn Leu Tyr Gln Tyr Pro Leu Asn
            1235   1240   1245
Pro Leu Gln Gln Ile Asp Pro Met Gly Leu Leu Gln Thr Trp Asp Asp
            1250   1255   1260
Ala Arg Ser Gly Ala Cys Thr Gly Gly Val Cys Gly Val Leu Ser Arg
1265   1270   1275   1280
Ile Ile Gly Pro Ser Lys Phe Asp Ser Thr Ala Asp Ala Ala Leu Asp
            1285   1290   1295
Ala Leu Lys Glu Thr Gln Asn Arg Ser Leu Cys Asn Asp Met Glu Tyr
            1300   1305   1310
Ser Gly Ile Val Cys Lys Asp Thr Asn Gly Lys Tyr Phe Ala Ser Lys
            1315   1320   1325
Ala Gln Thr Asp Asn Leu Arg Lys Glu Ser Tyr Pro Leu Lys Arg Lys
            1330   1335   1340
Cys Pro Thr Gly Thr Asp Arg Val Ala Ala Tyr His Thr His Gly Ala
1345   1350   1355   1360
Arg Ser His Gly Asp Tyr Val Asp Glu Phe Phe Ser Ser Ser Asp Lys
            1365   1370   1375
Asn Leu Val Arg Ser Lys Asp Asn Asn Leu Glu Ala Phe Tyr Leu Ala
            1380   1385   1390
Thr Pro Asp Gly Arg Phe Glu Ala Leu Asn Asn Lys Gly Glu Tyr Ile
            1395   1400   1405
Phe Ile Arg Asn Ser Val Pro Gly Leu Ser Ser Val Cys Ile Pro Tyr
            1410   1415   1420
His Asp
1425

        (210) 341
        (211) 170
        (212) PRT
        (213) E. Coli

        (400) 341
Met Lys Tyr Ser Ser Ile Phe Ser Met Leu Ser Phe Phe Ile Leu Phe
  1   5   10   15
Ala Cys Asn Glu Thr Ala Val Tyr Gly Ser Asp Glu Asn Ile Ile Phe
            20   25   30
Met Arg Tyr Val Glu Lys Leu His Leu Asp Lys Tyr Ser Val Lys Asn
        3   40   45
Thr Val Lys Thr Glu Thr Met Ala Ile Gln Leu Ala Glu Ile Tyr Val
        50   55   60
Arg Tyr Arg Tyr Gly Glu Arg Ile Ala Glu Glu Glu Lys Pro Tyr Leu

Ile Thr Glu Leu Pro Asp Ser Trp Val Val Glu Gly Ala Lys Leu Pro
                    85   90   95
Tyr Glu Val Ala Gly Gly Val Phe Ile Ile Glu Ile Asn Lys Lys Asn
                    100   105   110
Gly Cys Val Leu Asn Phe Leu His Ser Lys
            115   120

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<210> 342
<211> 236
<212> PRT
<213> E. Coli

<400> 342
```

Met Leu Ala Leu Met Asp Ala Asp Gly Asn Ile Ala Trp Ser Gly Glu
1   5   10   15
Tyr Asp Glu Trp Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Leu
                    20   25   30
His Gln Pro Tyr Arg Leu Pro Gly Gln Gln Tyr Asp Lys Glu Ser Gly
            35   40   45
Leu Tyr Tyr Asn Arg Asn Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr
            50   55   60
Ile Thr Gln Asp Pro Ile Gly Leu Glu Gly Gly Trp Ser Leu Tyr Ala
65   70   75   80
Tyr Pro Leu Asn Pro Val Asn Gly Ile Asp Pro Leu Gly Leu Ser Pro
                    85   90   95
Ala Asp Val Ala Leu Ile Arg Arg Lys Asp Gln Leu Asn His Gln Arg
                    100   105   110
Ala Trp Asp Ile Leu Ser Asp Thr Tyr Glu Asp Met Lys Arg Leu Asn
                    115   120   125
Leu Gly Gly Thr Asp Gln Phe Phe His Cys Met Ala Phe Cys Arg Val
            130   135   140
Ser Lys Leu Asn Asp Ala Gly Val Ser Arg Ser Ala Lys Gly Leu Gly
145   150   155   160
Tyr Glu Lys Glu Ile Arg Asp Tyr Gly Leu Asn Leu Phe Gly Met Tyr
                        165   170   175
Gly Arg Lys Val Lys Leu Ser His Ser Glu Met Ile Glu Asp Asn Lys
                    180   185   190
Lys Asp Leu Ala Val Asn Asp His Gly Leu Thr Cys Pro Ser Thr Thr
                195   200   205
Asp Cys Ser Asp Arg Cys Ser Asp Tyr Ile Asn Pro Glu His Lys Lys
            210   215   220
Thr Ile Lys Ala Leu Gln Asp Ala Gly Tyr Leu Lys
225   230   235

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<210> 343
<211> 87
<212> PRT
<213> E. Coli

<400> 343
```

Met Leu Ala Ile Ser Ser Asn Leu Ser Lys Met Ile Ile Phe Ile Phe
1   5   10   15
Ala Ile Ile Ile Ile Val Val Leu Cys Val Ile Thr Tyr Leu Tyr Leu
                    20   25   30

Tyr Lys Asp Glu Ser Leu Val Ser Lys His Tyr Ile Asn Tyr Met Ala
        35   40   45
Ile Pro Glu Asn Asp Gly Val Phe Thr Trp Leu Pro Asp Phe Phe Pro
        50   55   60
His Val Ala Val Asp Ile Ser Ile Tyr Thr Asn Val Glu Asp Asp Tyr
65   70   75   80
Phe Phe Leu Ile Phe Pro
                    85

        <210> 344
        <211> 85
        <212> PRT
        <213> E. Coli

        <400> 344
Met Arg Ala Arg Glu Gln Val Ala Lys Ile Val Ser Lys Asn Asp Pro
1   5   10   15
Asp Thr Lys Lys Val Trp Cys Lys Tyr Gly Lys Ile Pro Gly Gln Gly
                20   25   30
Asp Gly Val Asn Leu Phe Phe Val Gly Gln Ile Asn Val Thr His Tyr
            35   40   45
Phe Ile Thr Asn Ile Gly Ala Gly Leu Pro Asp Ala Cys Ala Glu
        50   55   60

        <210> 345
        <211> 167
        <212> PRT
        <213> E. Coli

        <400> 345
Met Pro Gly Asn Ser Pro His Tyr Gly Arg Trp Pro Gln His Asp Phe
1   5   10   15
Thr Ser Leu Lys Lys Leu Arg Pro Gln Ser Val Thr Ser Arg Ile Gln
                20   25   30
Pro Gly Ser Asp Val Ile Val Cys Ala Glu Met Asp Glu Gln Trp Gly
            35   40   45
Tyr Val Gly Ala Lys Ser Arg Gln Arg Trp Leu Phe Tyr Ala Tyr Asp
        50   55   60
Ser Leu Arg Lys Thr Val Val Ala His Val Phe Gly Glu Arg Thr Met
65   70   75   80
Ala Thr Leu Gly Arg Leu Met Ser Leu Leu Ser Pro Phe Asp Val Val
                85   90   95
Ile Trp Met Thr Asp Gly Trp Pro Leu Tyr Glu Ser Arg Leu Lys Gly
            100   105   110
Lys Leu His Val Ile Ser Lys Arg Tyr Thr Gln Arg Ile Glu Arg His
        115   120   125
Asn Leu Asn Leu Arg Gln His Leu Ala Arg Leu Gly Arg Lys Ser Leu
        130   135   140
Ser Phe Ser Lys Ser Val Glu Leu His Asp Lys Val Ile Gly His Tyr
145   150   155   160
Leu Asn Ile Lys His Tyr Gln
                165

```
Met Ala Ser Val Ser Ile Ser Cys Pro Ser Cys Ser Ala Thr Asp Gly
1               5                   10                  15
Val Val Arg Asn Gly Lys Ser Thr Ala Gly His Gln Arg Tyr Leu Cys
            20                  25                  30
Ser His Cys Arg Lys Thr Trp Gln Leu Gln Phe Thr Tyr Thr Ala Ser
        35                  40                  45
Gln Pro Gly Thr His Gln Lys Ile Ile Asp Met Ala Met Asn Gly Val
        50                  55                  60
Gly Cys Arg Ala Thr Ala Arg Ile Met Gly Val Gly Leu Asn Thr Ile
65                  70                  75                  80
Leu Arg His Leu Lys Asn Ser Gly Arg Ser Arg
                    85                  90
```

```
Met Met Thr Lys Thr Gln Ile Asn Lys Leu Ile Lys Met Met Asn Asp
1               5                   10                  15
Leu Asp Tyr Pro Phe Glu Ala Pro Leu Lys Glu Ser Phe Ile Glu Ser
            20                  25                  30
Ile Ile Gln Ile Glu Phe Asn Ser Asn Ser Thr Asn Cys Leu Glu Lys
        35                  40                  45
Leu Cys Asn Glu Val Ser Ile Leu Phe Lys Asn Gln Pro Asp Tyr Leu
        50                  55                  60
Thr Phe Leu Arg Ala Met Asp Gly Phe Glu Val Asn Gly Leu Arg Leu
65                  70                  75                  80
Phe Ser Leu Ser Ile Pro Glu Pro Ser Val Lys Asn Leu Phe Ala Val
                    85                  90                  95
Asn Gly Phe Tyr Arg Asn Asn Arg Asp Phe Ile Asn Pro Asp Leu Gln
                100                 105                 110
Glu Arg Leu Val Ile Gly Asp Tyr Ser Ile Ser Ile Phe Thr Tyr Asp
            115                 120                 125
Ile Lys Gly Asp Ala Ala Asn Leu Leu Ile
            130                 135
```

```
Met Ser Asn Ile Val Tyr Leu Thr Val Thr Gly Glu Gln Gln Gly Ser
1               5                   10                  15
Ile Ser Ala Gly Cys Gly Thr Ser Glu Ser Thr Gly Asn Arg Trp Gln
```

```
              20              25              30
Ser Gly His Glu Asp Glu Ile Phe Thr Phe Ser Leu Leu Asn Asn Ile
        35          40              45
Asn Asn Thr Gly Leu Gly Ser Gln Phe His Gly Ile Thr Phe Cys Lys
    50          55              60
Leu Ile Asp Lys Ser Thr Pro Leu Phe Ile Asn Ser Ile Asn Asn Asn
65              70              75              80
Glu Gln Leu Phe Met Gly Phe Asp Phe Tyr Arg Ile Asn Arg Phe Gly
                85              90              95
Arg Leu Glu Lys Tyr Tyr Tyr Ile Gln Leu Arg Gly Ala Phe Leu Ser
            100             105             110
Ala Ile His His Gln Ile Ile Glu Asn Gln Leu Asp Thr Glu Thr Ile
            115             120             125
Thr Ile Ser Tyr Glu Phe Ile Leu Lys Gln His Leu Ile Ala Asn Thr
        130             135             140
Glu Phe Ser Tyr Leu Ala Leu Pro Glu Asn Tyr Asn Arg Leu Phe Leu
145             150             155             160
Pro Asn Ser Lys Asn Gln Thr Asn Asn Arg Phe Lys Thr Leu Asn Ser
            165             170             175
Lys Ala Ile Gly Arg Leu Leu Ala Ala Gly Gly Val Tyr Asn Gly Asn
            180             185             190
Ile Glu Gly Phe Arg Asp Thr Ala Glu Lys Leu Gly Gly Asp Ala Ile
            195             200
Lys Gly Tyr Asp Gln Ile Leu Asn Glu Lys Thr Ala Gly Ile Ala Ile
    210             215             220
Ala Thr Ala Ser Ile Leu Leu Thr Lys Arg Ser Asn Val Asp Thr Tyr
225             230             235             240/241
Thr Glu Ile Asn Ser Tyr Leu Gly Lys Leu Arg Gly Gln Gln Lys Leu
            245             250             255
Leu Asp Gly Ile Asp Ile Ile Glu Ile Ile Tyr Ile Lys Arg Pro Ser
            260             265             270
Lys Asp Leu Ala Asn Leu Arg Lys Glu Phe Asn Lys Thr Val Arg Lys
            275             280             285
Asn Phe Leu Ile Lys Leu Ala Lys Thr Ser Glu Ala Ser Gly Arg Phe
        290             295             300
Asn Ala Glu Asp Leu Leu Arg Met Arg Lys Gly Asn Val Pro Leu Asn
305             310             315             320
Tyr Asn Val His His Lys Leu Ser Leu Asp Asp Gly Gly Thr Asn Asp
            325             330             335
Phe Gly Asn Leu Val Leu Ile Glu Asn Glu Pro Tyr His Lys Val Phe
            340             345             350
Thr Asn Met Gln Ser Arg Ile Ala Lys Gly Ile Leu Val Gly Glu Ser
        355             360             365
Lys Ile Thr Pro Trp Ala Ile Pro Ser Gly Ser Ile Tyr Pro Pro Met
370             375             380
Lys Asn Ile Met Arg His Thr Lys
385             390


        <211> 443
        <211> ???
        <212> PRT
        <213> E. Coli

        <400> 44
Met Val Leu Ala Leu Asn Tyr Asn Met His Gly Val Asn Ile Arg Ser
```

```
        1               5                   10                  15
Glu Asn Ala Ala Lys Pro His Thr Met Pro Ser Arg Tyr Leu Cys Glu
                    20                  25                  30
Tyr Ile Arg Ser Ile Glu Lys Asn Gly His Ala Leu Asp Phe Gly Cys
            35                  40                  45
Gly Lys Leu Arg Tyr Ser Asp Glu Leu Ile Ser Lys Phe Asp Glu Val
        50                  55                  60
Thr Phe Leu Asp Ser Lys Arg Gln Leu Glu Arg Glu Gln Ile Ile Arg
65                  70                  75                  80
Gly Ile Lys Thr Lys Ile Ile Asp Tyr Val Pro Arg Tyr Tyr Lys Asn
                    85                  90                  95
Ala Asn Thr Val Ala Phe Glu Asp Val Asp Lys Ile Ile Gly Gly Tyr
                100                 105                 110
Asp Phe Ile Leu Cys Ser Asn Val Leu Ser Ala Val Pro Cys Arg Asp
            115                 120                 125
Thr Ile Asp Lys Ile Val Leu Ser Ile Lys Arg Leu Leu Lys Ser Gly
        130                 135                 140
Gly Glu Thr Leu Ile Val Asn Gln Tyr Lys Ser Ser Tyr Phe Lys Lys
145                 150                 155                 160
Tyr Glu Thr Gly Arg Lys His Leu Tyr Gly Tyr Ile Tyr Lys Asn Ser
                    165                 170                 175
Lys Ser Val Ser Tyr Tyr Gly Leu Leu Asp Glu Leu Ala Val Gln Glu
                180                 185                 190
Ile Tyr Ser Ser His Gly Leu Glu Ile Leu Lys Ser Trp Ser Lys Ala
            195                 200                 205
Gly Ser Ser Tyr Val Thr Val Gly Ser Cys Asn Ala Ile
        210                 215                 220
```

```
    <210> 61
    <211> 224
    <212> PRT
    <213> E. Coli

    <400> 56
```

```
Met Asn Asn Met Phe Glu Pro Pro Lys Asn Tyr Asn Glu Met Leu Pro
 1               5                   10                  15
Lys Leu His Lys Ala Thr Phe Leu Asn Thr Leu Ile Tyr Cys Ile Leu
            20                  25                  30
Leu Val Ile Tyr Glu Tyr Ile Pro Leu Ile Thr Leu Pro Thr Lys Tyr
            35                  40                  45
Val Pro Pro Ile Lys Asp His Glu Ser Phe Ile Asn Trp Ala Leu Ser
        50                  55                  60
Phe Gly Ile Leu Pro Cys Ala Phe Ala Ile Phe Ala Tyr Leu Ile Ser
61                  70                  75                  80
Gly Ala Leu Asp Leu His Asn Asn Ala Ala Lys Leu Leu Arg Val Arg
                85                  90                  95
Tyr Leu Trp Asp Lys His Leu Ile Ile Lys Pro Leu Ser Arg Arg Ala
                100                 105                 110
Gly Val Asn Arg Lys Leu Asn Lys Asp Glu Ala His Asn Val Met Ser
            115                 120                 125
Asn Leu Tyr Tyr Pro Glu Val Arg Lys Ile Glu Asp Lys His Tyr Ile
        130                 135                 140
Glu Leu Phe Trp Asn Lys Val Tyr Tyr Phe Trp Ile Phe Phe Glu Phe
145                 150                 155                 160
Ser Ile Ile Ala Leu Ile Ser Phe Leu Ile Ile Phe Phe Cys Lys Gln
                165                 170                 175
```

Met Asp Ile Phe His Val Glu Gly Ser Leu Leu Ser Leu Phe Phe Phe
       130   145   190

Val Ile Leu Ser Phe Ser Val Ser Gly Ile Ile Phe Ala Leu Thr Val
       145   200   205

Lys Pro Arg Thr Glu Ser Gln Val Gly Lys Ile Pro Asp Asp Lys Ile
       210   215   220

Lys Glu Phe Phe Thr Lys Asn Asn Ile Asn
225   230

<210> 251
<211> 44
<212> PRT
<213> E. Coli

<400> 251

Met Phe Thr Ile Asn Ala Glu Val Arg Lys Glu Gln Gly Lys Gly Ala
1   5   10   15

Ser Arg Arg Leu Arg Ala Ala Asn Lys Phe Pro Ala Ile Ile Tyr Gly
       20   25   30

Gly Lys Glu Ala Pro Leu Ala Ile Glu Leu Asp His Asp Lys Val Met
       35   40   45

Asn Met Gln Ala Lys Ala Glu Phe Tyr Ser Glu Val Leu Thr Ile Val
       50   55   60

Val Asp Gly Lys Glu Ile Lys Val Lys Ala Gln Asp Val Gln Arg His
60   70   75   80

Pro Tyr Lys Pro Lys Leu Gln His Ile Asp Phe Val Arg Ala
             85   90

<210> 252
<211> 458
<212> PRT
<213> E. Coli

<400> 252

Met Val Leu Phe Tyr Arg Ala His Trp Arg Asp Tyr Lys Asn Asp Gln
1   5   10   15

Val Arg Ile Met Met Asn Leu Thr Thr Leu Thr His Arg Asp Ala Leu
       20   25   30

Cys Leu Asn Ala Arg Phe Thr Ser Arg Glu Glu Ala Ile His Ala Leu
       35   40   45

Thr Gln Arg Leu Ala Ala Leu Gly Lys Ile Ser Ser Thr Glu Gln Phe
       50   55   60

Leu Glu Glu Val Tyr Arg Arg Glu Ser Leu Gly Pro Thr Ala Leu Gly
45   70   75   80

Glu Gly Leu Ala Val Pro His Gly Lys Thr Ala Ala Val Lys Glu Ala
             85   90   95

Ala Phe Ala Val Ala Thr Leu Ser Glu Pro Leu Gln Trp Glu Gly Val
             100   105   110

Asp Gly Pro Glu Ala Val Asp Leu Val Val Leu Leu Ala Ile Pro Pro
             115   120   125

Asn Glu Ala Gly Thr Thr His Met Gln Leu Leu Thr Ala Leu Thr Thr
        130   135   140

Arg Leu Ala Asp Asp Glu Ile Arg Ala Arg Ile Gln Ser Ala Thr Thr
145   150   155   160

Pro Asp Glu Leu Leu Ser Ala Leu Asp Asp Lys Gly Gly Thr Gln Pro
                165   170   175

Ser Ala Ser Phe Ser Asn Ala Pro Thr Ile Val Cys Val Thr Ala Cys
                180   185   190

Pro Ala Gly Ile Ala His Thr Tyr Met Ala Ala Glu Tyr Leu Glu Lys
                195   200   205

Ala Gly Arg Lys Leu Gly Val Asn Val Tyr Val Glu Lys Gln Gly Ala
        210   215   220

Asn Gly Ile Glu Gly Arg Leu Thr Ala Asp Gln Leu Asn Ser Ala Thr
225   230   235   240

Ala Cys Ile Pro Ala Ala Glu Val Ala Ile Lys Glu Ser Glu Arg Phe
                245   250   255

Asn Gly Ile Pro Ala Leu Ser Val Pro Val Ala Glu Pro Ile Arg His
                260   265   270

Ala His Ala Leu Ile Gln Gln Ala Leu Thr Leu Lys Arg Ser Asp Glu
        275   280   285

Thr Arg Thr Val Gln Gln Asp Thr Gln Pro Val Lys Ser Val Lys Thr
        290   295   300

Glu Leu Lys Gln Ala Leu Leu Ser Gly Ile Ser Phe Ala Val Pro Leu
305   310   315   320

Ile Val Ala Gly Gly Thr Val Leu Ala Val Ala Val Leu Leu Ser Gln
                325   330   335

Ile Phe Gly Leu Gln Asp Leu Phe Asn Glu Gln Asn Ser Trp Leu Trp
                340   345   350

Met Tyr Arg Lys Leu Gly Gly Gly Leu Leu Gly Ile Leu Met Val Pro
            355   360   365

Val Leu Ala Ala Tyr Thr Ala Tyr Ser Leu Ala Asp Lys Pro Ala Leu
        370   375   380

Ala Pro Gly Pro Ala Ala Gly Leu Ala Ala Asn Met Ile Gly Ser Gly
385   390   395   400

Phe Leu Gly Ala Val Val Gly Gly Leu Ile Ala Gly Tyr Leu Met Arg
                405   410   415

Trp Val Lys Asn His Leu Arg Leu Ser Ser Lys Phe Asn Gly Phe Leu
            420   425   430

Thr Phe Tyr Leu Tyr Pro Val Leu Gly Thr Leu Gly Ala Gly Ser Leu
            435   440   445

Met Leu Phe Val Val Gly Glu Pro Val Ala Trp Ile Asn Asn Ser Leu
        450   455   460

Thr Ala Trp Leu Asn Gly Leu Ser Gly Ser Asn Ala Leu Leu Leu Gly
465   470   475   480

Ala Ile Leu Gly Phe Met Tyr Ser Phe Asp Leu Gly Gly Pro Val Asn
                485   490   495

Lys Ala Ala Tyr Ala Phe Cys Leu Gly Ala Met Ala Asn Gly Val Tyr
                500   505   510

Gly Pro Tyr Ala Ile Phe Ala Ser Val Lys Met Val Ser Ala Phe Thr
            515   520   525

Val Thr Ala Ser Thr Met Leu Ala Pro Arg Leu Phe Lys Glu Phe Glu
        530   535   540

Ile Gly Thr Gly Lys Ser Thr Trp Leu Leu Gly Leu Ala Gly Ile Thr
545   550   555   560

Glu Gly Ala Ile Pro Met Ala Ile Glu Asp Pro Leu Arg Val Ile Gly
                565   570   575

Ser Phe Val Leu Gly Ser Met Val Thr Gly Ala Ile Val Gly Ala Met
            580   585   590

Asn Ile Gly Leu Ser Thr Pro Gly Ala Gly Ile Phe Ser Leu Phe Leu
            595   600   605

Leu His Asp Asn Gly Ala Gly Gly Val Met Ala Ala Ile Gly Trp Phe

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```
        610                     615                      620
Gly Ala Ala Leu Val Gly Ala Ala Ile Ser Thr Ala Ile Leu Leu Met
625                     630                      635                      640
Trp Arg Arg His Ala Val Lys His Gly Asn Tyr Leu Thr Asp Gly Val
                    645                      650                      655

Met Pro
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```
        <210> 355
        <211> 577
        <212> PRT
        <213> E. Coli

        <400> 355
Met Lys Ala Val Ser Arg Val His Ile Thr Pro His Met His Trp Asp
  1                   5                       10                      15
Arg Glu Trp Tyr Phe Thr Thr Glu Glu Ser Arg Ile Leu Leu Val Asn
                    20                      25                      30
Asn Met Glu Glu Ile Leu Cys Arg Leu His Gln Asp Asn Glu Tyr Lys
                    35                      40                      45
Tyr Tyr Val Leu Asp Gly Gln Thr Ala Ile Leu Glu Asp Tyr Phe Ala
                    50                      55                      60
Val Lys Pro Glu Asn Lys Asp Arg Val Lys Lys Gln Val Glu Ala Gly
65                      70                      75                      80
Lys Leu Ile Ile Gly Pro Trp Tyr Thr Gln Thr Asp Thr Thr Ile Val
                    85                      90                      95
Ser Ala Gly Ser Ile Val Arg Asn Leu Met Tyr Gly Met Arg Asp Cys
                    100                     105                     110
Leu Ala Phe Gly Glu Pro Met Lys Ile Lys Tyr Leu Pro Asp Ser Phe
                    115                     120                     125
Gly Met Ser Gly Gln Leu Pro His Ile Tyr Asn Gly Phe Gly Ile Thr
                    130                     135                     140
Arg Thr Met Phe Trp Arg Gly Cys Ser Glu Arg His Gly Thr Asp Lys
145                     150                     155                     160
Thr Glu Phe Leu Trp Gln Ser Ser Asp Gly Ser Glu Val Thr Ala Gln
                    165                     170                     175
Val Leu Pro Leu Gly Tyr Ala Ile Gly Lys Tyr Leu Pro Ala Asp Glu
                    180                     185                     190
Asn Gly Leu Arg Lys Arg Leu Asp Ser Tyr Phe Asp Val Leu Glu Lys
                    195                     200                     205
Ala Ser Val Thr Lys Glu Ile Leu Leu Pro Asn Gly His Asp Gln Met
210                     215                     220
Pro Leu Gln Gln Asn Ile Phe Glu Val Met Asp Lys Leu Arg Glu Ile
225                     230                     235                     240
Tyr Pro Gln Arg Lys Phe Val Met Ser Arg Phe Glu Glu Val Phe Glu
                    245                     250                     255
Lys Ile Glu Ala Gln Arg Asp Asn Leu Ala Thr Leu Lys Gly Glu Phe
                    260                     265                     270
Ile Asp Gly Lys Tyr Met Arg Val His Arg Thr Ile Gly Ser Thr Arg
                    275                     280                     285
Met Asp Ile Lys Ile Ala His Ala Arg Ile Glu Asn Lys Ile Val Asn
290                     295                     300
Leu Leu Glu Pro Leu Ala Thr Leu Ala Trp Thr Leu Gly Phe Glu Tyr
305                     310                     315                     320
His His Gly Leu Leu Glu Lys Met Trp Lys Glu Ile Leu Lys Asn His
                    325                     330                     335
```

```
Ala His Asp Ser Ile Gly Cys Cys Cys Ser Asp Lys Val His Arg Glu
        340             345             350
Ile Val Ala Arg Phe Glu Leu Ala Glu Asp Met Ala Asp Asn Leu Ile
        355             360             365
Arg Phe Tyr Met Arg Lys Ile Ala Asp Asn Met Pro Gln Ser Asp Ala
    370             375             380
Asp Lys Leu Val Leu Phe Asn Leu Met Pro Trp Pro Arg Glu Glu Val
385             390             395             400
Ile Asn Thr Thr Val Arg Leu Arg Ala Ser Gln Phe Asn Leu Arg Asp
                405             410             415
Asp Arg Gly Gln Pro Val Pro Tyr Phe Ile Arg His Ala Arg Glu Ile
            420             425             430
Asp Pro Gly Leu Ile Asp Arg Gln Ile Val His Tyr Gly Asn Tyr Asp
            435             440             445
Pro Phe Met Glu Phe Asp Ile Gln Ile Asn Gln Ile Val Pro Ser Met
        450             455             460
Gly Tyr Arg Thr Leu Tyr Ile Glu Ala Asn Gln Pro Gly Asn Val Ile
465             470             475             480
Ala Ala Lys Ser Asp Ala Glu Gly Ile Leu Glu Asn Ala Phe Trp Gln
                485             490             495
Ile Ala Leu Asn Glu Asp Gly Ser Leu Gln Leu Val Asp Lys Asp Ser
            500             505             510
Gly Val Arg Tyr Asp Arg Val Leu Gln Ile Glu Glu Ser Ser Asp Asp
        515             520             525
Gly Asp Glu Tyr Asp Tyr Ser Pro Ala Lys Glu Glu Trp Val Ile Thr
        530             535             540
Ala Ala Asn Ala Lys Pro Gln Cys Asp Ile Ile His Glu Ala Trp Gln
545             550             555             560
Ser Arg Ala Val Ile Arg Tyr Asp Met Ala Val Pro Leu Asn Leu Ser
                565             570             575
Glu Arg Ser Ala Arg Gln Ser Thr Gly Arg Val Gly Val Val Leu Val
            580             585             590
Val Thr Leu Ser His Asn Ser Arg Arg Ile Asp Val Asp Ile Asn Leu
        595             600             605
Asp Asn Gln Ala Asp Asp His Arg Leu Arg Val Leu Val Pro Thr Pro
    610             615             620
Phe Asn Thr Asp Ser Val Leu Ala Asp Thr Gln Phe Gly Ser Leu Thr
625             630             635             640
Arg Pro Val Asn Asp Ser Ala Met Asn Asn Trp Gln Gln Glu Gly Trp
                645             650             655
Lys Glu Ala Pro Val Pro Val Trp Asn Met Leu Asn Tyr Val Ala Leu
            660             665             670
Gln Glu Gly Arg Asn Gly Met Ala Val Phe Ser Glu Gly Leu Arg Glu
        675             680             685
Phe Glu Val Ile Gly Glu Glu Lys Lys Thr Phe Ala Ile Thr Leu Leu
        690             695             700
Arg Gly Val Gly Leu Leu Gly Lys Glu Asp Leu Leu Leu Arg Pro Gly
705             710             715             720
Arg Pro Ser Gly Ile Lys Met Pro Val Pro Asp Ser Gln Leu Arg Gly
                725             730             735
Leu Leu Ser Cys Arg Leu Ser Leu Leu Ser Tyr Thr Gly Thr Pro Thr
            740             745             750
Ala Ala Gly Val Ala Gln Gln Ala Arg Ala Trp Leu Thr Pro Val Gln
        755             760             765
Cys Tyr Asn Lys Ile Pro Trp Asp Val Met Lys Leu Asn Lys Ala Gly
    770             775             780
Phe Asn Val Pro Glu Ser Tyr Ser Leu Leu Lys Met Pro Pro Val Gly
```

```
785                   790                   795                   800
Cys Leu Ile Ser Ala Leu Lys Lys Ala Glu Asp Arg Gln Glu Val Ile
                805                   810                   815
Leu Arg Leu Phe Asn Pro Ala Glu Ser Ala Thr Cys Asp Ala Thr Val
                820                   825                   830
Ala Phe Ser Arg Glu Val Ile Ser Lys Ser Glu Thr Met Met Asp Glu
                835                   840                   845
His Ile Thr Thr Glu Glu Asn Gln Gly Ser Asn Leu Ser Gly Pro Phe
                850                   855                   860
Leu Pro Gly Gln Ser Arg Thr Phe Ser Tyr Arg Leu Ala
865                   870                   375


        <210> 204
        <211> 315
        <212> PRT
        <213> E. Coli

        <400> 204
Met Met Leu Asp Ile Val Glu Leu Ser Arg Leu Gln Phe Ala Leu Thr
1                   5                   10                   15
Ala Met Tyr His Phe Leu Phe Val Pro Leu Thr Leu Gly Met Ala Phe
                20                   25                   30
Leu Leu Ala Ile Met Glu Thr Val Tyr Val Leu Ser Gly Lys Gln Ile
                35                   40                   45
Tyr Lys Asp Met Thr Lys Phe Trp Gly Lys Leu Phe Gly Ile Asn Phe
                50                   55                   60
Ala Leu Gly Val Ala Thr Gly Leu Thr Met Glu Phe Gln Phe Gly Thr
65                   70                   75                   80
Asn Trp Ser Tyr Tyr Ser His Tyr Val Gly Asp Ile Phe Gly Ala Pro
                85                   90                   95
Leu Ala Ile Glu Gly Leu Met Ala Phe Phe Leu Glu Ser Thr Phe Val
                100                  105                  110
Gly Leu Phe Phe Phe Gly Trp Asp Arg Leu Gly Lys Val Gln His Met
                115                  120                  125
Cys Val Thr Trp Leu Val Ala Leu Gly Ser Asn Leu Ser Ala Leu Trp
        130                  135                  140
Ile Leu Val Ala Asn Gly Trp Met Gln Asn Pro Ile Ala Ser Asp Phe
145                  150                  155                  160
Asn Thr Glu Thr Met Arg Met Glu Met Val Ser Phe Ser Glu Leu Val
                165                  170                  175
Leu Asn Pro Val Ala Gln Val Lys Phe Val His Thr Val Ala Ser Gly
                180                  185                  190
Tyr Val Thr Gly Ala Met Phe Ile Leu Gly Ile Ser Ala Trp Tyr Met
                195                  200                  205
Leu Lys Gly Arg Asp Phe Ala Phe Ala Lys Arg Ser Phe Ala Ile Ala
        210                  215                  220
Ala Ser Phe Gly Met Ala Ala Val Leu Ser Val Ile Val Leu Gly Asp
225                  230                  235                  240
Glu Ser Gly Tyr Glu Met Gly Asp Val Gln Lys Thr Lys Leu Ala Ala
                245                  250                  255
Ile Glu Ala Glu Trp Glu Thr Gln Pro Ala Pro Ala Ala Phe Thr Leu
                250                  265                  270
Phe Gly Ile Pro Asp Gln Glu Glu Glu Thr Asn Lys Phe Ala Ile Gln
        275                  280                  285
Ile Pro Tyr Ala Leu Gly Ile Ile Ala Thr Arg Ser Val Asp Thr Pro
        290                  295                  300
```
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```
Val Ile Gly Leu Lys Glu Leu Met Val Gln His Glu Glu Arg Ile Arg
305             310              315              320
Asn Gly Met Lys Ala Tyr Ser Leu Leu Glu Gln Leu Arg Ser Gly Ser
                325              330              335
Thr Asp Gln Ala Val Arg Asp Gln Phe Asn Ser Met Lys Lys Asp Leu
                340              345              350
Gly Tyr Gly Leu Leu Leu Lys Arg Tyr Thr Pro Asn Val Ala Asp Ala
                355              360              365
Thr Glu Ala Gln Ile Gln Gln Ala Thr Lys Asp Ser Ile Pro Arg Val
370              375              380
Ala Pro Leu Tyr Pro Ala Phe Arg Ile Met Val Ala Cys Gly Phe Leu
381              390              395              400
Leu Leu Ala Ile Ile Ala Leu Ser Phe Trp Ser Val Ile Arg Asn Arg
                405              410              415
Ile Gly Glu Lys Lys Trp Leu Leu Arg Ala Ala Leu Tyr Gly Ile Pro
                420              425              430
Leu Pro Trp Ile Ala Val Glu Ala Gly Trp Phe Val Ala Glu Tyr Gly
                435              440              445
Arg Gln Pro Trp Ala Ile Gly Glu Val Leu Pro Thr Ala Val Ala Asn
         450              455              460
Ser Ser Leu Thr Ala Gly Asp Leu Ile Phe Ser Met Val Leu Ile Cys
465              470              475              480
Gly Leu Tyr Thr Leu Phe Leu Val Ala Glu Leu Phe Leu Met Phe Lys
                485              490              495
Phe Ala Arg Leu Gly Pro Ser Ser Leu Lys Thr Gly Arg Tyr His Phe
                501              505              510
Glu Gln Ser Ser Thr Thr Thr Gln Pro Ala Arg
                513              515


    <210> 335
    <211> 379
    <212> PRT
    <213> E. Coli


    <400> 335
Met Ile Asp Tyr Glu Val Leu Arg Phe Ile Trp Trp Leu Leu Val Gly
1               5               10              15
Val Leu Leu Ile Gly Phe Ala Val Thr Asp Gly Phe Asp Met Gly Val
        21              25              30
Gly Met Leu Thr Arg Phe Leu Gly Arg Asn Asp Thr Glu Arg Arg Ile
     36              40              45
Met Ile Asn Ser Ile Ala Pro His Trp Asp Gly Asn Gln Val Trp Leu
     50              56              61
Ile Thr Ala Gly Gly Ala Leu Phe Ala Ala Trp Pro Met Val Tyr Ala
65              70              75              81
Ala Ala Phe Ser Gly Phe Tyr Val Ala Met Ile Leu Val Leu Ala Ser
                83              90              95
Leu Phe Phe Arg Pro Val Gly Phe Asp Tyr Arg Ser Lys Ile Glu Glu
                100             105             110
Thr Arg Trp Arg Asn Met Trp Asp Trp Gly Ile Phe Ile Gly Ser Phe
        115             120             125
Val Pro Pro Leu Val Ile Gly Val Ala Phe Gly Asn Leu Leu Gln Gly
     130             135             140
Val Pro Phe Asn Val Asp Glu Tyr Leu Arg Leu Tyr Tyr Thr Gly Asn
145             150             155             160
Phe Phe Gln Leu Leu Asn Pro Phe Gly Leu Leu Ala Gly Val Val Ser
```

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```
                    165                 170                 175
Val Gly Met Ile Ile Thr Gln Gly Ala Thr Tyr Leu Gln Met Arg Thr
        180                 185                 190
Val Gly Glu Leu His Leu Arg Thr Arg Ala Thr Ala Gln Val Ala Ala
            195                 200                 205
Leu Val Thr Leu Val Cys Phe Ala Leu Ala Gly Val Trp Val Met Tyr
            210                 215                 220
Gly Ile Asp Gly Tyr Val Val Lys Ser Thr Met Asp His Tyr Ala Ala
    225                 230                 235                 240
Ser Asn Pro Leu Asn Lys Glu Val Val Arg Glu Ala Gly Ala Trp Leu
                245                 250                 255
Val Asn Phe Asn Asn Thr Pro Ile Leu Trp Ala Ile Pro Ala Leu Gly
            260                 265                 270
Val Val Leu Pro Leu Leu Thr Ile Leu Thr Ala Arg Met Asp Lys Ala
        275                 280                 285
Ala Trp Ala Phe Val Phe Ser Ser Leu Thr Leu Ala Cys Ile Ile Leu
            290                 295                 300
Thr Ala Gly Ile Ala Met Phe Pro Phe Val Met Pro Ser Ser Thr Met
    305                 310                 315                 320
Met Asn Ala Ser Leu Thr Met Trp Asp Ala Thr Ser Ser Gln Leu Thr
                325                 330                 335
Leu Asn Val Met Thr Trp Val Ala Val Val Leu Val Pro Ile Ile Leu
            340                 345                 350
Leu Tyr Thr Ala Trp Cys Tyr Trp Lys Met Phe Gly Arg Ile Thr Lys
            355                 360                 365
Glu Arg Ile Glu Arg Asn Thr His Ser Leu Tyr
        370                 375
```

```
   <210> 456
   <211> 456
   <213> PRT
   213  E. Coli

   <400> 456
```

```
Met Glu Leu Ser Ser Leu Thr Ala Val Ser Pro Val Asp Gly Arg Tyr
1               5                   10                  15
Gly Arg Lys Val Ser Ala Leu Arg Gly Ile Phe Ser Glu Tyr Gly Leu
            20                  25                  30
Leu Lys Phe Arg Val Gln Val Glu Val Arg Trp Leu Gln Lys Leu Ala
        40                  30                  45
Ala His Ala Ala Ile Lys Glu Val Pro Ala Phe Ala Ala Asp Ala Ile
    50                  55                  60
Gly Tyr Leu Asp Ala Ile Val Ala Ser Phe Ser Glu Glu Asp Ala Ala
75                  70                  75                  80
Arg Ile Lys Thr Ile Glu Arg Thr Thr Asn His Asp Val Lys Ala Val
            85                  90                  95
Glu Tyr Phe Leu Lys Glu Lys Val Ala Glu Ile Pro Glu Leu His Ala
            100                 105                 110
Val Ser Glu Phe Ile His Phe Ala Cys Thr Ser Glu Asp Ile Asn Asn
            115                 120                 125
Leu Ser His Ala Leu Met Leu Lys Thr Ala Arg Asp Glu Val Ile Leu
        130                 135                 140
Pro Tyr Trp Arg Gln Leu Ile Asp Gly Ile Lys Asp Leu Ala Val Gln
145                 150                 155                 160
Tyr Arg Asp Ile Pro Leu Leu Ser Arg Thr His Gly Gln Pro Ala Thr
                165                 170                 175
```

Pro Ser Thr Ile Gly Lys Glu Met Ala Asn Val Ala Tyr Arg Met Glu
                150   185   190
Arg Gln Tyr Arg Gln Leu Asn Gln Val Glu Ile Leu Gly Lys Ile Asn
            195   200   205
Gly Ala Val Gly Asn Tyr Asn Ala His Ile Ala Ala Tyr Pro Glu Val
    210   215   210
Asp Trp His Gln Phe Ser Glu Glu Phe Val Thr Ser Leu Gly Ile Gln
225   230   235   240
Trp Asn Pro Tyr Thr Thr Gln Ile Glu Pro His Asp Tyr Ile Ala Glu
            245   250   255
Leu Phe Asp Lys Val Ala Arg Phe Asn Thr Ile Leu Ile Asp Phe Asp
            260   265   270
Arg Asp Val Trp Gly Tyr Ile Ala Leu Asn His Phe Lys Gln Lys Thr
    275   280   285
Ile Ala Gly Glu Ile Gly Ser Ser Thr Met Pro His Lys Val Asn Pro
    290   295   300
Ile Asp Phe Glu Asn Ser Glu Gly Asn Leu Gly Leu Ser Asn Ala Val
305   310   315   320
Leu Gln His Leu Ala Ser Lys Leu Pro Val Ser Arg Trp Gln Arg Asp
            325   330   335
Leu Thr Asp Ser Thr Val Leu Arg Asn Leu Gly Val Gly Ile Gly Tyr
            341   345   351
Ala Leu Ile Ala Tyr Gln Ser Thr Leu Lys Gly Val Ser Lys Leu Glu
    355   361   365
Val Asn Arg Asp His Leu Leu Asp Glu Leu Asp His Asn Trp Glu Val
    370   375   380
Leu Ala Glu Pro Ile Gln Thr Val Met Arg Arg Tyr Gly Ile Glu Lys
385   390   395   400
Pro Tyr Glu Lys Leu Lys Glu Leu Thr Arg Gly Lys Arg Val Asp Ala
            405   410   415
Glu Gly Met Lys Gln Phe Ile Asp Gly Leu Ala Leu Pro Glu Glu Glu
            410   420   430
Lys Ala Arg Leu Lys Ala Met Thr Pro Ala Asn Tyr Ile Gly Arg Ala
            435   440   445
Ile Thr Met Val Asp Glu Leu Lys
    450   455

    <210> 3-7
    <211> 71
    <212> PRT
    <213> E. Coli

    <400> 357

Met Leu Ile Leu Thr Arg Arg Val Gly Glu Thr Leu Met Ile Gly Asp
1   5   10   15
Glu Val Thr Val Thr Val Leu Gly Val Lys Gly Asn Gln Val Arg Ile
            21   25   30
Gly Val Asn Ala Pro Lys Glu Val Ser Val His Arg Glu Glu Ile Tyr
        35   41   45
Gln Arg Ile Gln Ala Glu Lys Ser Gln Gln Ser Ser Tyr
    50   55   60

    <210> 3-8
    <211> 63
    <212> RNA

<210> E. Coli

<400> 258
ggugagggg: chaagaggcu gaaggcgcuc cccugcuaag ggaguaugcg gucaaaagcu   60
gcauccgugi uucgaaugcc cgccucaccg ca   83

<211> 353
<211> 200
<212> PRT
<213> E. Coli

<400> 259

Met	Lys	Asn	Lys	Ala	Asp	Asn	Lys	Lys	Arg	Asn	Phe	Leu	Thr	His	Ser
1				5					10					15	
Glu	Ile	Gln	Ser	Leu	Leu	Lys	Ala	Ala	Asn	Thr	Gly	Pro	His	Ala	Ala
			20					25				30			
Arg	Asn	Tyr	Cys	Leu	Thr	Leu	Leu	Cys	Phe	Ile	His	Gly	Phe	Arg	Ala
		35				40					45				
Ser	Glu	Ile	Cys	Arg	Leu	Arg	Ile	Ser	Asp	Ile	Asp	Leu	Lys	Ala	Lys
	50					55				60					
Cys	Ile	Tyr	Ile	His	Arg	Leu	Lys	Lys	Gly	Phe	Ser	Thr	Thr	His	Pro
65					70				75					80	
Leu	Leu	Asn	Lys	Glu	Val	Gln	Ala	Leu	Lys	Asn	Trp	Leu	Ser	Ile	Arg
			85					90					95		
Thr	Ser	Tyr	Pro	His	Ala	Glu	Ser	Glu	Trp	Val	Phe	Leu	Ser	Arg	Lys
			100					115				110			
Gly	Asn	Pro	Leu	Ser	Arg	Gln	Gln	Phe	Tyr	His	Ile	Ile	Ser	Thr	Ser
			115				120					125			
Gly	Gly	Asn	Ala	Gly	Leu	Ser	Leu	Glu	Ile	His	Pro	His	Met	Leu	Arg
	131				135				140						
His	Ser	Cys	Gly	Phe	Ala	Leu	Ala	Asn	Met	Gly	Ile	Asp	Thr	Arg	Leu
145				150				155					160		
Ile	Gln	Asp	Tyr	Leu	Gly	His	Arg	Asn	Ile	Arg	His	Thr	Val	Trp	Tyr
			165				170					175			
Thr	Ala	Ser	Asn	Ala	Gly	Arg	Phe	Tyr	Gly	Ile	Trp	Asp	Arg	Ala	Arg
			180				185				190				
Gly	Arg	Gln	Arg	His	Ala	Val	Leu								
	195				200										

<210> 360
<211> 145
<212> PRT
<213> E. Coli

<400> 260

Met	Ser	Lys	Arg	Arg	Tyr	Leu	Thr	Gly	Lys	Glu	Val	Gln	Ala	Met	Met
1				5				10					15		
Gln	Ala	Val	Cys	Tyr	Gly	Ala	Thr	Gly	Ala	Arg	Asp	Tyr	Cys	Leu	Ile
			20				25					31			
Leu	Leu	Ala	Tyr	Arg	His	Gly	Met	Arg	Ile	Ser	Glu	Leu	Leu	Asp	Leu
		3				40					45				
His	Tyr	Gln	Asp	Leu	Asp	Leu	Asn	Glu	Gly	Arg	Ile	Asn	Ile	Arg	Arg
	50					55				60					
Leu	Lys	Asn	Gly	Phe	Ser	Thr	Val	His	Pro	Leu	Arg	Phe	Asp	Glu	Arg
65					70				75					80	

Glu Ala Val Glu Arg Trp Thr Gln Glu Arg Ala Asn Trp Lys Gly Ala
                85   90   95

Asp Arg Thr Asp Ala Ile Phe Ile Ser Arg Arg Gly Ser Arg Leu Ser
            100   115   110

Arg Gln Gln Ala Tyr Arg Ile Ile Arg Asp Ala Gly Ile Glu Ala Gly
        115   120   125

Thr Val Thr Gln Thr His Pro His Met Leu Arg His Ala Cys Gly Tyr
    130   135   140

Glu Leu Ala Glu Arg Gly Ala Asp Thr Arg Leu Ile Gln Asp Tyr Leu
145   150   155   160

Gly His Arg Asn Ile Arg His Thr Val Arg Tyr Thr Ala Ser Asn Ala
            165   170   175

Ala Arg Phe Ala Gly Leu Trp Glu Arg Asn Asn Leu Ile Asn Glu Lys
        180   185   190

Leu Lys Arg Glu Gln Val
        195

Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
1   5   10   15

Ser Ser Thr Ala Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr
        20   25   30

Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
        35   40   45

Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
    50   55   60

Leu Ala Gln Gln Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65   70   75   80

Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
            85   90   95

Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
        100   105   110

Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
        115   120   125

Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
    130   135   140

Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145   150   155   160

Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr
            165   170   175

Phe Lys Val Gln Tyr Gln
        180

Met Leu Leu Met Arg Met Arg Pro Ser Arg Phe Ser Ile Asn Asn Leu
1   5   10   15

Pro Arg Phe Arg Asp Val Ile Thr Gly Arg Asp Ala His Pro Cys Ala
      20   25   30

Ile Lys Ile Thr Met Lys Arg Lys Arg Leu Phe Leu Leu Ala Ser Leu
      35   40   45

Leu Pro Met Phe Ala Leu Ala Gly Asn Lys Trp Asn Thr Thr Leu Pro
      50   55   60

Gly Gly Asn Met Gln Phe Gln Gly Val Ile Ile Ala Glu Thr Cys Arg
65   70   75   80

Ile Glu Ala Gly Asp Lys Gln Met Thr Val Asn Met Gly Gln Ile Ser
      85   90   95

Ser Asn Arg Phe His Ala Val Gly Glu Asp Ser Ala Pro Val Pro Phe
      100   105   110

Val Ile His Leu Arg Glu Cys Ser Thr Val Val Ser Glu Arg Val Gly
      115   120   125

Val Ala Phe His Gly Val Ala Asp Gly Lys Asn Pro Asp Val Leu Ser
      130   135   140

Val Gly Glu Gly Pro Gly Ile Ala Thr Asn Ile Gly Val Ala Leu Phe
145   150   155   160

Asp Asp Glu Gly Asn Leu Val Pro Ile Asn Arg Pro Pro Ala Asn Trp
      165   170   175

Lys Arg Leu Tyr Ser Gly Ser Thr Ser Leu His Phe Ile Ala Lys Tyr
      180   185   190

Arg Ala Thr Gly Arg Arg Val Thr Gly Gly Ile Ala Asn Ala Gln Ala
      195   200   205

Trp Phe Ser Leu Thr Tyr Gln
210   215

<210> 3??
<211> 241
<212> PRT
<213> E. Coli

<400> 3??

Met Ser Asn Lys Asn Val Asn Val Arg Lys Ser Gln Glu Ile Thr Phe
1   5   10   15

Cys Leu Leu Ala Gly Ile Leu Met Phe Met Ala Met Met Val Ala Gly
      20   25   30

Arg Ala Gln Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro
      35   40   45

Ala Gly Gln Lys Gln Glu Gln Leu Ala Val Thr Asn Asn Asp Glu Asn
      50   55   60

Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys
65   70   75   80

Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys
      85   90   95

Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro
      100   105   110

Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser
      115   120   125

Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile
130   135   140

Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro
145   150   155   160

Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu
        165   170   175
Thr Leu Ile Asn Pro Thr Pro Tyr Tyr Leu Thr Val Thr Glu Leu Asn
        180   185   190
Ala Gly Thr Arg Val Leu Glu Asn Ala Leu Val Pro Pro Met Gly Glu
        195   200   205
Ser Thr Val Lys Leu Pro Ser Asp Ala Gly Ser Asn Ile Thr Tyr Arg
        210   215   220
Thr Ile Asn Asp Tyr Gly Ala Leu Thr Pro Lys Met Thr Gly Val Met
        225   230   235   240
Glu

<210> 364
<211> 578
<212> PRT
<213> E. Coli

<400> 364

Met Ser Tyr Leu Asn Leu Arg Leu Tyr Gln Arg Asn Thr Gln Cys Leu
1   5   10   15
His Ile Arg Lys His Arg Leu Ala Gly Phe Phe Val Arg Leu Val Val
        20   25   30
Ala Cys Ala Phe Ala Ala Gln Ala Pro Leu Ser Ser Ala Asp Leu Tyr
        35   40   45
Phe Asn Pro Arg Phe Leu Ala Asp Asp Pro Gln Ala Val Ala Asp Leu
        50   55   60
Ser Arg Phe Glu Asn Gly Gln Glu Leu Pro Pro Gly Thr Tyr Arg Val
65   70   75   80
Asp Ile Tyr Leu Asn Asn Gly Tyr Met Ala Thr Arg Asp Val Thr Phe
        85   90   95
Asn Thr Gly Asp Ser Glu Gln Gly Ile Val Pro Cys Leu Thr Arg Ala
        100   105   110
Gln Leu Ala Ser Met Gly Leu Asn Thr Ala Ser Val Ala Gly Met Asn
        115   120   125
Leu Leu Ala Asp Asp Ala Cys Val Pro Leu Thr Thr Met Val Gln Asp
        130   135   140
Ala Thr Ala His Leu Asp Val Gly Gln Gln Arg Leu Asn Leu Thr Ile
145   150   155   160
Pro Gln Ala Phe Met Ser Asn Arg Ala Arg Gly Tyr Ile Pro Pro Glu
        165   170   175
Leu Trp Asp Pro Gly Ile Asn Ala Gly Leu Leu Asn Tyr Asn Phe Ser
        180   185   190
Gly Asn Ser Val Gln Asn Arg Ile Gly Gly Asn Ser His Tyr Ala Tyr
        195   200   205
Leu Asn Leu Gln Ser Gly Leu Asn Ile Gly Ala Trp Arg Leu Arg Asp
        210   215   220
Asn Thr Thr Trp Ser Tyr Asn Ser Ser Asp Arg Ser Ser Gly Ser Lys
        225   230   235   240
Asn Lys Trp Gln His Ile Asn Thr Trp Leu Glu Arg Asp Ile Ile Pro
        245   250   255
Leu Arg Ser Arg Leu Thr Leu Gly Asp Gly Tyr Thr Gln Gly Asp Ile
        260   265   270
Phe Asp Gly Ile Asn Phe Arg Gly Ala Gln Leu Ala Ser Asp Asp Asn
        275   280   285
Met Leu Pro Asp Ser Gln Arg Gly Phe Ala Pro Val Ile His Gly Ile

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      290                 295                 300
Ala Arg Gly Thr Ala Gln Val Thr Ile Lys Gln Asn Gly Tyr Asp Ile
305                 310                 315                 320
Tyr Asn Ser Thr Val Pro Pro Gly Pro Phe Thr Ile Asn Asp Ile Tyr
                325                 330                 335
Ala Ala Gly Asn Ser Gly Asp Leu Gln Val Thr Ile Lys Glu Ala Asp
                340                 345                 350
Gly Ser Thr Gln Ile Phe Thr Val Pro Tyr Ser Ser Val Pro Leu Leu
                355                 360                 365
Gln Arg Glu Gly His Thr Arg Tyr Ser Ile Thr Ala Gly Glu Tyr Arg
                370                 375                 380
Ser Gly Asn Ala Gln Gln Glu Lys Thr Arg Phe Phe Gln Ser Thr Leu
385                 390                 395                 400
Leu His Gly Leu Pro Ala Gly Trp Thr Ile Tyr Gly Gly Thr Gln Leu
                405                 410                 415
Ala Asp Arg Tyr Arg Ala Phe Asn Phe Gly Ile Gly Lys Asn Met Gly
                420                 425                 430
Ala Leu Gly Ala Leu Ser Val Asp Met Thr Gln Ala Asn Ser Thr Leu
                435                 440                 445
Pro Asp Asp Ser Gln His Asp Gly Gln Ser Val Arg Phe Leu Tyr Asn
                450                 455                 460
Lys Ser Leu Asn Glu Ser Gly Thr Asn Ile Gln Leu Val Gly Tyr Arg
465                 470                 475                 480
Tyr Ser Thr Ser Gly Tyr Pro Asn Phe Ala Asp Thr Thr Tyr Ser Arg
                485                 490                 495
Met Asn Gly Tyr Asn Ile Glu Thr Gln Asp Gly Val Ile Gln Val Lys
                500                 505                 510
Pro Lys Phe Thr Asp Tyr Tyr Asn Leu Ala Tyr Asn Lys Arg Gly Lys
                515                 520                 525
Leu Gln Leu Thr Val Thr Gln Gln Leu Gly Arg Thr Ser Thr Leu Tyr
                530                 535                 540
Leu Ser Gly Ser His Gln Thr Tyr Trp Gly Thr Ser Asn Val Asp Gln
545                 550                 555                 560
Gln Phe Gln Ala Gly Leu Asn Thr Ala Phe Glu Asp Ile Asn Trp Thr
                565                 570                 575
Leu Ser Tyr Ser Leu Thr Lys Asn Ala Trp Gln Lys Gly Arg Asp Gln
                580                 585                 590
Met Leu Ala Leu Asn Val Asn Ile Pro Phe Ser His Trp Leu Arg Ser
                595                 600                 605
Asp Ser Lys Ser Gln Trp Arg His Ala Ser Ala Ser Tyr Ser Met Ser
610                 615                 620
His Asp Leu Asn Gly Arg Met Thr Asn Leu Ala Gly Val Tyr Gly Thr
625                 630                 635                 640
Leu Leu Gln Asp Asn Asn Leu Ser Tyr Ser Val Gln Thr Gly Tyr Ala
                645                 650                 655
Gly Gly Gly Asp Gly Asn Ser Gly Ser Thr Gly Tyr Ala Thr Leu Asn
                660                 665                 670
Tyr Arg Gly Gly Tyr Gly Asn Ala Asn Ile Gly Tyr Ser His Ser Asp
                675                 680                 685
Asp Ile Lys Gln Leu Tyr Tyr Gly Val Ser Gly Gly Val Leu Ala His
                690                 695                 700
Ala Asn Gly Val Thr Leu Gly Gln Pro Leu Asn Asp Thr Val Val Leu
705                 710                 715                 720
Val Lys Ala Pro Gly Ala Lys Asp Ala Lys Val Glu Asn Gln Thr Gly
                725                 730                 735
Val Arg Thr Asp Trp Arg Gly Tyr Ala Val Leu Pro Tyr Ala Thr Glu
                740                 745                 750
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Tyr Arg Glu Asn Arg Val Ala Leu Asp Thr Asn Thr Leu Ala Asp Asn
    755   760   765

Val Asp Leu Asp Asn Ala Val Ala Asn Val Val Pro Thr Arg Gly Ala
    770   775   780

Ile Val Arg Ala Glu Phe Lys Ala Arg Val Gly Ile Lys Leu Leu Met
785   790   795   800

Thr Leu Thr His Asn Asn Lys Pro Leu Pro Phe Gly Ala Met Val Thr
            805   810   815

Ser Glu Ser Ser Gln Ser Ser Gly Ile Val Ala Asp Asn Gly Gln Val
            820   825   830

Tyr Leu Ser Gly Met Pro Leu Ala Gly Lys Val Gln Val Lys Trp Gly
            835   840   845

Glu Glu Glu Asn Ala His Cys Val Ala Asn Tyr Gln Leu Pro Pro Glu
            850   855   860

Ser Gln Gln Gln Leu Leu Thr Gln Leu Ser Ala Glu Cys Arg
865   870   875

<210> 365
<211> 376
<212> PRT
<213> E. Coli

<400> 365

Met Arg Asn Lys Pro Phe Tyr Leu Leu Cys Ala Phe Leu Trp Leu Ala
1   5   10   15

Val Ser His Ala Leu Ala Ala Asp Ser Thr Ile Thr Ile Arg Gly Tyr
        20   25   30

Val Arg Asp Asn Gly Cys Ser Val Ala Ala Glu Ser Thr Asn Phe Thr
        35   40   45

Val Asp Leu Met Glu Asn Ala Ala Lys Gln Phe Asn Asn Ile Gly Ala
    50   55   60

Thr Thr Pro Val Val Pro Phe Arg Ile Leu Leu Ser Pro Cys Gly Asn
65   70   75   80

Ala Val Ser Ala Val Lys Val Gly Phe Thr Gly Val Ala Asp Ser His
        85   90   95

Asn Ala Asn Leu Leu Ala Leu Glu Asn Thr Val Ser Ala Ala Ser Gly
        100   105   110

Leu Gly Ile Gln Leu Leu Asn Glu Gln Gln Asn Gln Ile Pro Leu Asn
        115   120   125

Ala Pro Ser Ser Ala Leu Ser Trp Thr Thr Leu Thr Pro Gly Lys Pro
    130   135   140

Asn Thr Leu Asn Phe Tyr Ala Arg Leu Met Ala Thr Gln Val Pro Val
145   150   155   160

Thr Ala Gly His Ile Asn Ala Thr Ala Thr Phe Thr Leu Glu Tyr Gln
        165   170   175

<210> 366
<211> 167
<212> PRT
<213> E. Coli

<400> 366

Met Lys Trp Cys Lys Arg Gly Tyr Val Leu Ala Ala Ile Leu Ala Leu
1   5   10   15

Ala Ser Ala Thr Ile Gln Ala Ala Asp Val Thr Ile Thr Val Asn Gly
        20   25   30

Lys Val Val Ala Lys Pro Cys Thr Val Ser Thr Thr Asn Ala Thr Val
        35   40   45

Asp Leu Gly Asp Leu Tyr Ser Phe Ser Leu Met Ser Ala Gly Ala Ala
        50   55   60

Ser Ala Trp His Asp Val Ala Leu Glu Leu Thr Asn Cys Pro Val Gly
65   70   75   80

Thr Ser Arg Val Thr Ala Ser Phe Ser Gly Ala Ala Asp Ser Thr Gly
        85   90   95

Tyr Tyr Lys Asn Gln Gly Thr Ala Gln Asn Ile Gln Leu Glu Leu Gln
        100   105   110

Asp Asp Ser Gly Asn Thr Leu Asn Thr Gly Ala Thr Lys Thr Val Gln
        115   120   125

Val Asp Asp Ser Ser Gln Ser Ala His Phe Pro Leu Gln Val Arg Ala
        130   135   140

Leu Thr Val Asn Gly Gly Ala Thr Gln Gly Thr Ile Gln Ala Val Ile
145   150   155   160

Ser Ile Thr Tyr Thr Tyr Ser
        165

<210> 567
<211> 300
<212> PRT
<213> E. Coli

<400> 567

Met Lys Arg Val Ile Thr Leu Phe Ala Val Leu Leu Met Gly Trp Ser
1   5   10   15

Val Asn Ala Trp Ser Phe Ala Cys Lys Thr Ala Asn Gly Thr Ala Ile
        20   25   30

Pro Ile Gly Gly Gly Ser Ala Asn Val Tyr Val Asn Leu Ala Pro Val
        35   40   45

Val Asn Val Gly Gln Asn Leu Val Val Asp Leu Ser Thr Gln Ile Phe
        50   55   60

Cys His Asn Asp Tyr Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln
65   70   75   80

Arg Gly Ser Ala Tyr Gly Gly Val Leu Ser Asn Phe Ser Gly Thr Val
        85   90   95

Lys Tyr Ser Gly Ser Ser Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro
        100   105   110

Arg Val Val Tyr Asn Ser Arg Thr Asp Lys Pro Trp Pro Val Ala Leu
        115   120   125

Tyr Leu Thr Pro Val Ser Ser Ala Gly Gly Val Ala Ile Lys Ala Gly
        130   135   140

Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser
145   150   155   160

Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val
                165   170   175

Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr
        180   185   190

Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys
        195   200   205

Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp
210   215   220

Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln
225   230   235   240

Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn
                    245   250   255

Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly
                260   265   270

Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn
            275   280   285

Val Gln Ser Ile Ile Gly Val Thr Phe Val Tyr Gln
            290   295   300

    <210> 365
    <211> 5.1
    <212> PRT
    <213> E. Coli

    <400> 365

Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys
1   5   10   15

Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu
                20   25   30

Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp
            35   40   45

Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile
        50   55   60

Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn
65   70   75   80

Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu
                85   90   95

Ser Asn Asp Ser Arg Leu Thr Gly Cys Glu Arg Ser Pro Phe Glu Ser
                100   105   110

Tyr Gly Asn Cys Ser Leu Thr Gly Gln Arg Thr Leu Arg Asn Phe Pro
            115   120   125

Gly Cys Arg His Gly Pro Cys Arg Ser Cys Ala Gly Val Leu Gly Ser
        130   135   140

Ser Gln Lys Glu Arg Pro Ala Ser Leu Pro Gly Ser Ser Arg Lys Ile
145   150   155   160

Val Arg Lys Ser Val Leu Ser Ala Ala Ser Val Leu Leu Asp Lys Ser
                165   170   175

Cys Gln Ala Arg Ala Ser Ser Ser Ile Ser Met Asn Thr Lys Ile Arg
            180   185   190

Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu Ile Gly Ala Gly Ala Ser
            195   200   205

Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp Glu Lys Glu Gly Asn His
        210   215   220

Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile Trp Thr Ile Cys Arg Gly
225   230   235   240

Ala Thr Val Val Asp Gly Lys Thr Val Phe Pro Asn Met Lys Leu Ser
                245   250   255

Lys Glu Lys Cys Asp Gln Val Asn Ala Ile Glu Arg Asp Lys Ala Leu
            260   265   270

Ala Trp Val Glu Arg Asn Ile Lys Val Pro Leu Thr Glu Pro Gln Lys
        275   280   285

Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn Ile Gly Pro Gly Lys Cys
    290   295   300

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Phe Pro Ser Thr Phe Tyr Lys Arg Leu Asn Ala Gly Asp Arg Lys Gly
305 310 315 320

Ala Cys Glu Ala Ile Arg Trp Trp Ile Lys Asp Gly Gly Arg Asp Cys
325 330 335

Arg Ile Arg Ser Asn Asn Cys Tyr Gly Gln Val Ile Arg Arg Asp Gln
340 345 350

Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu Gln Ile Arg Tyr Ser Trp
355 360 365

Phe Phe Ser Cys Cys Gln Asp Leu Ser Ser Glu Met Ser Gly Ala Thr
370 375 380

Glu Asp Gly Lys Lys Asn Gly Arg Asn Val Met Leu Pro His Tyr His
385 390 395 400

Lys Arg Met Leu Asn Leu Leu Leu Glu Leu Asn Arg Gly Glu Leu Pro
405 410 415

Val Met Arg Leu Leu Lys Met Arg Asn Arg Asn Leu Leu Lys Phe Leu
420 425 430

Pro Gly Leu Leu Ile Cys Leu Ile Val Leu Thr Ser Cys Val Pro Lys
435 440 445

Gln Lys Asn Met Pro Tyr Ala Leu Thr Gln Arg Ser Ile Pro Gln Ile
450 455 460

Leu Pro Leu Pro Ser Glu Ala Lys Gln Pro Lys Pro Pro Lys Glu Cys
465 470 475 481

Ser Pro Thr Cys Ser Glu Ile Leu Gln Gln Lys Leu Ser Phe Met Leu
485 490 495

Lys Leu Leu Thr Asn Ala Thr Ser Gln Gly Leu Val Asn Arg Ser Met
500 505 511

Asn Leu Glu Ile Lys Ser Ile Lys Cys
520

<210> 362
<211> 1??
<212> PRT
<213> E. Coli

<400> 362

Met Asn Thr Lys Ile Arg Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu
1 5 10 15

Ile Gly Ala Gly Ala Ser Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp
20 25 30

Glu Lys Gln Gly Asn His Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile
35 40 45

Trp Thr Ile Cys Arg Gly Ala Thr Val Val Asp Gly Lys Thr Val Phe
50 55 60

Pro Asn Met Lys Leu Ser Lys Glu Lys Cys Asp Gln Val Asn Ala Ile
65 70 75 80

Glu Arg Asp Lys Ala Leu Ala Trp Val Glu Arg Asn Ile Lys Val Pro
85 90 95

Leu Thr Glu Pro Gln Lys Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn
100 105 110

Ile Gly Pro Gly Lys Cys Phe Pro Ser Thr Phe Tyr Lys Arg Leu Asn
115 120 125

Ala Gly Asp Arg Lys Gly Ala Cys Glu Ala Ile Arg Trp Trp Ile Lys
130 135 140

Asp Gly Gly Arg Asp Cys Arg Ile Arg Ser Asn Asn Cys Tyr Gly Gln
145 150 155 160

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Val Ile Arg Arg Asp Gln Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu
                    165   170   175
Gln

<210> 370
<211> 103
<212> PRT
<213> E. Coli

<400> 370
Met Thr Gln Asp Tyr Glu Leu Val Val Lys Gly Val Arg Asn Phe Glu
1   5   10   15
Asn Lys Val Thr Val Thr Val Ala Leu Gln Asp Lys Glu Arg Phe Asp
                    20   25   30
Gly Glu Ile Phe Asp Leu Asp Val Ala Met Asp Arg Val Glu Gly Ala
                35   40   45
Ala Leu Glu Phe Tyr Glu Ala Ala Arg Arg Ser Val Arg Gln Val
            50   55   60
Phe Leu Gln Val Ala Glu Lys Leu Ser Glu Lys Val Glu Ser Tyr Leu
65   70   75   80
Gln His Gln Tyr Ser Phe Lys Ile Glu Asn Pro Ala Asn Lys His Glu
                85   90   95
Arg Pro His His Lys Tyr Leu
                100

<210> 371
<211> 96
<212> PRT
<213> E. Coli

<400> 371
Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys
1   5   10   15
Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu
                    20   25   30
Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp
                35   40   45
Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile
            50   55   60
Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn
65   70   75   80
Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu
                85   90   95

<210> 372
<211> 71
<212> PRT
<213> E. Coli

<400> 372
Met Ser Asn Lys Met Thr Gly Leu Val Lys Trp Phe Asn Ala Asp Lys

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        1               5                       10                      15
Gly Phe Gly Phe Ile Ser Pro Val Asp Gly Ser Lys Asp Val Phe Val
                20                      25                      30
His Phe Ser Ala Ile Gln Asn Asp Asn Tyr Arg Thr Leu Phe Glu Gly
                35                      40                      45
Gln Lys Val Thr Phe Ser Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
        50                      55                      60
Ala Asn Val Ile Ile Thr Asp
65                      70
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        <210> 373
        <211> 435
        <212> PRT
        <213> E. Coli

        <400> 373
Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
  1               5                       10                      15
Leu Thr Pro Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg
                20                      25                      30
Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
                35                      40                      45
Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
                50                      55                      60
Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
65                      70                      75                      80
Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
                        85                      90                      95
Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
                100                     105                     110
Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
                115                     120                     125
Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
        130                     135                     140
Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
145                     150                     155                     160
Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met
                165                     170                     175
His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His
                180                     185                     190
Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr
                195                     200                     205
Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly
        210                     215                     220
Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln
225                     230                     235                     240
Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg
                245                     250                     255
Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr
                260                     265                     270
Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu
                275                     280                     285
His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg
        290                     295                     300
Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr
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305                310                315                320
Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg
                  325                330                335
Ser His


        <210> 374
        <211> 157
        <212> PRT
        <213> E. Coli

        <400> 374
Met Val Tyr Ile Ile Ile Val Ser His Gly His Glu Asp Tyr Ile Lys
1                 5                 10                15
Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile
                  20                25                30
Val Arg Asp Asn Lys Asp Ser Leu Leu Leu Lys Gln Ile Cys Gln His
                  35                40                45
Tyr Ala Gly Leu Asp Tyr Ile Ser Gly Gly Val Tyr Gly Phe Gly His
        50                55                60
Asn Asn Asn Ile Ala Val Ala Tyr Val Lys Glu Lys Tyr Arg Pro Ala
65                70                75                80
Asp Asp Asp Tyr Ile Leu Phe Leu Asn Pro Asp Ile Ile Met Lys His
                  85                90                95
Asp Asp Leu Leu Thr Tyr Ile Lys Tyr Val Glu Ser Lys Arg Tyr Ala
        100               105               110
Phe Ser Thr Leu Cys Leu Phe Arg Asp Glu Ala Lys Ser Leu His Asp
        115               120               125
Tyr Ser Val Arg Lys Phe Pro Val Leu Ser Asp Phe Ile Val Ser Phe
        130               135               140
Met Leu Gly Ile Lys Glu Gly Ala Asn Lys Ser Leu Ile
145               150               155


        <210> 375
        <211> 371
        <212> PRT
        <213> E. Coli

        <400> 375
Met Gly Lys Ser Ile Val Val Val Ser Ala Val Asn Phe Thr Thr Gly
1                 5                 10                15
Gly Pro Phe Thr Ile Leu Lys Lys Phe Leu Ala Ala Thr Asn Asn Lys
                  20                25                30
Glu Asn Val Ser Phe Ile Ala Leu Val His Ser Ala Lys Glu Leu Lys
                  35                40                45
Glu Ser Tyr Pro Trp Val Lys Phe Ile Glu Phe Pro Glu Val Lys Gly
        50                55                60
Ser Trp Leu Lys Arg Leu His Phe Glu Tyr Val Val Cys Lys Lys Leu
65                70                75                80
Ser Lys Glu Leu Asn Ala Thr His Trp Ile Cys Leu His Asp Ile Thr
                  85                90                95
Ala Asn Val Val Thr Lys Lys Arg Tyr Val Tyr Cys His Asn Pro Ala
        100               105               110
Pro Phe Tyr Lys Gly Ile Leu Phe Arg Glu Ile Leu Met Glu Pro Ser
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            115                        120                        125
Phe Phe Leu Phe Lys Met Leu Tyr Gly Leu Ile Tyr Lys Ile Asn Ile
    130                        135                        140
Lys Lys Asn Thr Ala Val Phe Val Gln Gln Phe Trp Met Lys Glu Lys
145                        150                        155                        160
Phe Ile Lys Lys Tyr Ser Ile Asn Asn Ile Ile Val Ser Arg Pro Glu
                        165                        170                        175
Ile Lys Leu Ser Asp Lys Ser Gln Leu Thr Asp Asp Asp Ser Gln Phe
                    180                        185                        190
Lys Asn Asn Pro Ser Glu Leu Thr Ile Phe Tyr Pro Ala Val Pro Arg
                195                        200                        205
Val Phe Lys Asn Tyr Glu Leu Ile Ile Ser Ala Ala Arg Lys Leu Lys
    210                        215                        220
Glu Gln Ser Asn Ile Lys Phe Leu Leu Thr Ile Ser Gly Thr Glu Asn
225                        230                        235                        240
Ala Tyr Ala Lys Tyr Ile Ile Ser Leu Ala Glu Gly Leu Asp Asn Val
                        245                        250                        255
His Phe Leu Gly Tyr Leu Asp Lys Glu Lys Ile Asp His Cys Tyr Asn
                    260                        265                        270
Ile Ser Asp Ile Val Cys Phe Pro Ser Arg Leu Glu Thr Trp Gly Leu
                275                        280                        285
Pro Leu Ser Glu Ala Lys Glu Arg Gly Lys Trp Val Leu Ala Ser Asp
    290                        295                        300
Phe Pro Phe Thr Arg Glu Thr Leu Gly Ser Tyr Glu Lys Lys Ala Phe
305                        310                        315                        320
Phe Asp Ser Asn Asn Asp Asp Met Leu Val Lys Leu Ile Ile Asp Phe
                        325                        330                        335
Lys Lys Gly Asn Leu Lys Lys Asp Ile Ser Asp Ala Asn Phe Ile Tyr
                340                        345                        350
Arg Asn Glu Asn Val Leu Val Gly Phe Asp Glu Leu Val Asn Phe Ile
            355                        360                        365
Thr Glu Glu His
    370
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    <210> 376
    <211> 196
    <211> PRT
    <213> E. Coli

    <400> 376
Met Ile Leu Lys Leu Ala Lys Arg Tyr Gly Leu Cys Gly Phe Ile Arg
1                   5                        10                        15
Leu Val Arg Asp Val Leu Leu Thr Arg Val Phe Tyr Arg Asn Cys Arg
                20                        25                        30
Ile Ile Arg Phe Pro Cys Tyr Ile Arg Asn Asp Gly Ser Ile Asn Phe
                35                        40                        45
Gly Glu Asn Phe Thr Ser Gly Val Gly Leu Arg Leu Asp Ala Phe Gly
            50                        55                        60
Arg Gly Val Ile Phe Phe Ser Asp Asn Val Gln Val Asn Asp Tyr Val
65                        70                        75                        80
His Ile Ala Ser Ile Glu Ser Val Thr Ile Gly Arg Asp Thr Leu Ile
                        85                        90                        95
Ala Ser Lys Val Phe Ile Thr Asp His Asn His Gly Ser Phe Lys His
                100                        105                        110
Ser Asp Pro Met Ser Ser Pro Asn Ile Pro Pro Asp Met Arg Thr Leu
            115                        120                        125
```

Glu Ser Ser Ala Val Val Ile Gly Gln Arg Val Trp Leu Gly Glu Asn
    130   135   140

Val Thr Val Leu Pro Gly Thr Ile Ile Gly Asn Gly Val Val Val Gly
145   150   155   160

Ala Asn Ser Val Val Arg Gly Ser Ile Pro Glu Asn Thr Val Ile Ala
                165   170   175

Gly Val Pro Ala Lys Ile Ile Lys Lys Tyr Asn His Glu Thr Lys Leu
            180   185   190

Trp Glu Lys Ala
        195

    <210> 377
    <211> 330
    <212> PRT
    <213> E. Coli

    <400> 377
Met Tyr Phe Leu Asn Asp Leu Asn Phe Ser Arg Arg Asp Ala Gly Phe
1   5   10   15

Lys Ala Arg Lys Asp Ala Leu Asp Ile Ala Ser Asp Tyr Glu Asn Ile
            20   25   30

Ser Val Val Asn Ile Pro Leu Trp Gly Gly Val Val Gln Arg Ile Ile
        35   40   45

Ser Ser Val Lys Leu Ser Thr Phe Leu Cys Gly Leu Glu Asn Lys Asp
    50   55   60

Val Leu Ile Phe Asn Phe Pro Met Ala Lys Pro Phe Trp His Ile Leu
65   70   75   80

Ser Phe Phe His Arg Leu Leu Lys Phe Arg Ile Val Pro Leu Ile His
                85   90   95

Asp Ile Asp Glu Leu Arg Gly Gly Gly Gly Ser Asp Ser Val Arg Leu
            100   105   110

Ala Thr Cys Asp Met Val Ile Ser His Asn Pro Gln Met Thr Lys Tyr
        115   120   125

Leu Ser Lys Tyr Met Ser Gln Asp Lys Ile Lys Asp Ile Lys Ile Phe
    130   135   140

Asp Tyr Leu Val Ser Ser Asn Val Glu His Arg Asp Val Thr Asp Lys
145   150   155   160

Gln Arg Gly Val Ile Tyr Ala Gly Asn Leu Ser Arg His Lys Cys Ser
                165   170   175

Phe Ile Tyr Thr Glu Gly Cys Asp Pro Thr Leu Phe Gly Val Asn Tyr
            180   185   190

Glu Asn Lys Asp Asn Pro Lys Tyr Leu Gly Ser Phe Asp Ala Gln Ser
        195   200   205

Pro Glu Lys Ile Asn Leu Pro Gly Met Gln Phe Gly Leu Ile Pro Asp
    210   215   220

Gly Asp Ser Val Glu Thr Cys Ser Gly Ala Phe Gly Asp Tyr Leu Lys
225   230   235   240

Phe Asn Asn Pro His Lys Thr Ser Leu Tyr Leu Ser Met Glu Leu Pro
                245   250   255

Val Phe Ile Trp Asp Lys Ala Ala Leu Ala Asp Phe Ile Val Asp Asn
            260   265   270

Arg Ile Gly Tyr Ala Val Gly Ser Ile Lys Glu Met Gln Glu Ile Val
        275   280   285

Asp Ser Met Thr Ile Glu Thr Tyr Lys Gln Ile Ser Glu Asn Thr Lys
    290   295   300

Ile Ile Ser Gln Lys Ile Arg Thr Gly Ser Tyr Phe Arg Asp Val Leu
305   310   315   320

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Glu Glu Val Ile Asp Asp Leu Lys Thr Arg
          325   330

<210> 373
<211> 393
<212> PRT
<213> E. Coli

<400> 373

Met Ile Tyr Leu Val Ile Ser Val Phe Leu Ile Thr Ala Phe Ile Cys
1   5   10   15

Leu Tyr Leu Lys Lys Asp Ile Phe Tyr Pro Ala Val Cys Val Asn Ile
        20   25   30

Ile Phe Ala Leu Val Leu Leu Gly Tyr Glu Ile Thr Ser Asp Ile Tyr
        35   40   45

Ala Phe Gln Leu Asn Asp Ala Thr Leu Ile Phe Leu Leu Cys Asn Val
      50   55   60

Leu Thr Phe Thr Leu Ser Cys Leu Leu Thr Glu Ser Val Leu Asp Leu
65   70   75   80

Asn Ile Arg Lys Val Asn Asn Ala Ile Tyr Ser Ile Pro Ser Lys Lys
        85   90   95

Val His Asn Val Gly Leu Leu Val Ile Ser Phe Ser Met Ile Tyr Ile
        100   105   110

Cys Met Arg Leu Ser Asn Tyr Gln Phe Gly Thr Ser Leu Leu Ser Tyr
        115   120   125

Met Asn Leu Ile Arg Asp Ala Asp Val Glu Asp Thr Ser Arg Asn Phe
      130   135   140

Ser Ala Tyr Met Gln Pro Ile Ile Leu Thr Thr Phe Ala Leu Phe Ile
145   150   155   160

Trp Ser Lys Lys Phe Thr Asn Thr Lys Val Ser Lys Thr Phe Thr Leu
        165   170   175

Leu Val Phe Ile Val Phe Ile Phe Ala Ile Ile Leu Asn Thr Gly Lys
        180   185   190

Gln Ile Val Phe Met Val Ile Ile Ser Tyr Ala Phe Ile Val Gly Val
        195   200   205

Asn Arg Val Lys His Tyr Val Tyr Leu Ile Thr Ala Val Gly Val Leu
210   215   220

Phe Ser Leu Tyr Met Leu Phe Leu Arg Gly Leu Pro Gly Gly Met Ala
225   230   235   240

Tyr Tyr Leu Ser Met Tyr Leu Val Ser Pro Ile Ile Ala Phe Gln Glu
        245   250   255

Phe Tyr Phe Gln Gln Val Ser Asn Ser Ala Ser Ser His Val Phe Trp
      260   265   270

Phe Phe Gln Arg Leu Met Gly Leu Leu Thr Gly Gly Val Ser Met Ser
        275   280   285

Leu His Lys Gln Phe Val Trp Val Gly Leu Pro Thr Asn Val Tyr Thr
      290   295   300

Ala Phe Ser Asp Tyr Val Tyr Ile Ser Ala Glu Leu Ser Tyr Leu Met
305   310   315   320

Met Val Ile His Gly Cys Ile Ser Gly Val Leu Trp Arg Leu Ser Arg
        325   330   335

Asn Tyr Ile Ser Val Lys Ile Phe Tyr Ser Tyr Phe Ile Tyr Thr Phe
        340   345   350

Ser Phe Ile Phe Tyr His Glu Ser Phe Met Thr Asn Ile Ser Ser Trp
        355   360   365

Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala

Gln Lys Ile Lys
395

<210> 379
<211> 367
<212> PRT
<213> E. Coli

<400> 379

Met Tyr Asp Tyr Ile Ile Val Gly Ser Gly Leu Phe Gly Ala Val Cys
1   5   10   15
Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys
                20   25   30
Arg Asn His Ile Gly Gly Asn Ala Tyr Thr Glu Asp Cys Glu Gly Ile
            30   40   45
Gln Ile His Lys Tyr Gly Ala His Ile Phe His Thr Asn Asp Lys Tyr
            50   55   60
Ile Trp Asp Tyr Val Asn Asp Leu Val Glu Phe Asn Arg Phe Thr Asn
65   70   75   80
Ser Pro Leu Ala Ile Tyr Lys Asp Lys Leu Phe Asn Leu Pro Phe Asn
                85   90   95
Met Asn Thr Phe His Gln Met Trp Gly Val Lys Asp Pro Gln Glu Ala
                100   105   110
Gln Asn Ile Ile Asn Ala Gln Lys Lys Lys Tyr Gly Asp Lys Val Pro
            115   120   125
Glu Asn Leu Glu Glu Gln Ala Ile Ser Leu Val Gly Glu Asp Leu Tyr
            130   135   140
Gln Ala Leu Ile Lys Gly Tyr Thr Glu Lys Gln Trp Gly Arg Ser Ala
145   150   155   160
Lys Glu Leu Pro Ala Phe Ile Ile Lys Arg Ile Pro Val Arg Phe Thr
                165   170   175
Phe Asp Asn Asn Tyr Phe Ser Asp Arg Tyr Gln Gly Ile Pro Val Gly
                180   185   190
Gly Tyr Thr Lys Leu Ile Glu Lys Met Leu Glu Gly Val Asp Val Lys
            195   200   205
Leu Gly Ile Asp Phe Leu Lys Asp Lys Asp Ser Leu Ala Ser Lys Ala
210   215   220
His Arg Ile Ile Tyr Thr Gly Pro Ile Asp Gln Tyr Phe Asp Tyr Arg
225   230   235   240
Phe Gly Ala Leu Glu Tyr Arg Ser Leu Lys Phe Glu Thr Glu Arg His
                245   250   255
Glu Phe Pro Asn Phe Gln Gly Asn Ala Val Ile Asn Phe Thr Asp Ala
                260   265   270
Asn Val Pro Tyr Thr Arg Ile Ile Glu His Lys His Phe Asp Tyr Val
            275   280   285
Glu Thr Lys His Thr Val Val Thr Lys Glu Tyr Pro Leu Glu Trp Lys
            290   295   300
Val Gly Asp Glu Pro Tyr Tyr Pro Val Asn Asp Asn Lys Asn Met Glu
305   310   315   320
Leu Phe Lys Lys Tyr Arg Glu Leu Ala Ser Arg Glu Asp Lys Val Ile
                325   330   335
Phe Gly Gly Arg Leu Ala Glu Tyr Lys Tyr Tyr Asp Met His Gln Val
            340   345   350
Ile Ser Ala Ala Leu Tyr Gln Val Lys Asn Ile Met Ser Thr Asp

<210> 430
<211> 371
<212> PRT
<213> E. Coli

<400> 430

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Met Phe Pro Lys Ile Met Asn Asp Glu Asn Phe Phe Lys Lys Ala Ala
1               5                   10                  15
Ala His Gly Glu Glu Pro Pro Leu Thr Pro Gln Asn Glu His Gln Arg
            20              25                  30
Ser Gly Leu Arg Phe Ala Arg Arg Val Arg Leu Pro Arg Ala Val Gly
        35              40                  45
Leu Ala Gly Met Phe Leu Pro Ile Ala Ser Thr Leu Val Ser His Pro
    50              55                  60
Pro Pro Gly Trp Trp Trp Leu Val Leu Val Gly Trp Ala Phe Val Trp
65              70                  75                  80
Pro His Leu Ala Trp Gln Ile Ala Ser Arg Ala Val Asp Pro Leu Ser
            85              90                  95
Arg Glu Ile Tyr Asn Leu Lys Thr Asp Ala Val Leu Ala Gly Met Trp
            100                 105                 110
Val Gly Val Met Gly Val Asn Val Leu Pro Ser Thr Ala Met Leu Met
        115                 120                 125
Ile Met Tyr Leu Asn Leu Met Gly Ala Gly Gly Pro Arg Leu Phe Val
        130                 135                 140
Ala Gly Leu Val Leu Met Val Val Ser Cys Leu Val Thr Leu Glu Leu
135             141                 153                 160
Thr Gly Ile Thr Val Ser Phe Asn Ser Ala Pro Leu Glu Trp Trp Leu
            165                 170                 175
Ser Leu Pro Ile Ile Val Ile Tyr Pro Leu Leu Phe Gly Trp Val Ser
        180                 185                 190
Tyr Gln Thr Ala Thr Lys Leu Ala Glu His Lys Arg Arg Leu Gln Val
        195                 200                 205
Met Ser Thr Arg Asp Gly Met Thr Gly Val Tyr Asn Arg Arg His Trp
    210                 215                 220
Glu Thr Met Leu Arg Asn Glu Phe Asp Asn Cys Arg Arg His Asn Arg
225                 230                 235                 240
Asp Ala Thr Leu Leu Ile Ile Asp Ile Asp His Phe Lys Ser Ile Asn
                245                 251                 255
Asp Thr Trp Gly His Asp Val Gly Asp Glu Ala Ile Val Ala Leu Thr
            260                 265                 270
Arg Gln Leu Gln Ile Thr Leu Arg Gly Ser Asp Val Ile Gly Arg Phe
            275                 280                 285
Gly Gly Asp Glu Phe Ala Val Ile Met Ser Gly Thr Pro Ala Glu Ser
            290                 295                 300
Ala Ile Thr Ala Met Leu Arg Val His Glu Gly Leu Asn Thr Leu Arg
305                 310                 315                 320
Leu Pro Asn Thr Pro Gln Val Thr Leu Arg Ile Ser Val Gly Val Ala
                325                 331                 335
Pro Leu Asn Pro Gln Met Ser His Tyr Arg Gln Trp Leu Lys Ser Ala
            340                 345                 351
Asp Leu Ala Leu Tyr Lys Ala Lys Lys Ala Gly Arg Asn Arg Thr Glu
            355                 360                 365
Val Ala Ala
370
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<210> 381
<211> 467
<212> PRT
<213> E. Coli

<400> 381

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Met Asp Val Asn Val Asp Gln Phe Asp Thr Glu Ala Phe Arg Thr Asp
 1               5                  10                  15

Lys Leu Glu Leu Thr Ser Gly Asn Ile Ala Asp His Asn Gly Asn Val
             10                  25                  30

Val Ser Gly Val Phe Asp Ile His Ser Ser Asp Tyr Val Leu Asn Ala
             35                  40                  45

Asp Leu Val Asn Asp Arg Thr Trp Asp Thr Ser Lys Ser Asn Tyr Gly
             50                  55                  60

Tyr Gly Ile Val Ala Met Asn Ser Asp Gly His Leu Thr Ile Asn Gly
 65                  70                  75                  80

Asn Gly Asp Val Asp Asn Gly Thr Glu Leu Asp Asn Ser Ser Val Asp
                  85                  90                  95

Asn Val Val Ala Ala Thr Gly Asn Tyr Lys Val Arg Ile Asp Asn Ala
             100                 105                 110

Thr Gly Ala Gly Ala Ile Ala Asp Tyr Lys Asp Lys Glu Ile Ile Tyr
             115                 120                 125

Val Asn Asp Val Asn Ser Asn Ala Thr Phe Ser Ala Ala Asn Lys Ala
             130                 135                 140

Asp Leu Gly Ala Tyr Thr Tyr Gln Ala Glu Gln Arg Gly Asn Pro Val
145                 150                 155                 160

Val Leu Gln Gln Met Glu Leu Thr Asp Tyr Ala Asn Met Ala Leu Ser
                  165                 170                 175

Ile Pro Ser Ala Asn Thr Asn Ile Trp Asn Leu Glu Gln Asp Thr Val
                  180                 185                 190

Gly Thr Arg Leu Thr Asn Ser Arg His Gly Leu Ala Asp Asn Gly Gly
             195                 200                 205

Ala Trp Val Ser Tyr Phe Gly Gly Asn Phe Asn Gly Asp Asn Gly Thr
             210                 215                 220

Ile Asn Tyr Asp Gln Asp Val Asn Gly Ile Met Val Gly Val Asp Thr
225                 230                 235                 240

Lys Ile Asp Gly Asn Asn Ala Lys Trp Ile Val Gly Ala Ala Ala Gly
                  245                 250                 255

Phe Ala Lys Gly Asp Met Asn Asp Arg Ser Gly Gln Val Asp Gln Asp
             260                 265                 270

Ser Gln Thr Ala Tyr Ile Tyr Ser Ser Ala His Phe Ala Asn Asn Val
             275                 280                 285

Phe Val Asp Gly Ser Leu Ser Tyr Ser His Phe Asn Asn Asp Leu Ser
             290                 295                 300

Ala Thr Met Ser Asn Gly Thr Tyr Val Asp Gly Ser Thr Asn Ser Asp
305                 310                 315                 320

Ala Trp Gly Phe Gly Leu Lys Ala Gly Tyr Asp Phe Lys Leu Gly Asp
             325                 330                 335

Ala Gly Tyr Val Thr Pro Tyr Gly Ser Val Ser Gly Leu Phe Gln Ser
             340                 345                 350

Gly Asp Asp Tyr Gln Leu Ser Asn Asp Met Lys Val Arg Gly Gln Ser
             355                 360                 365

Tyr Asp Ser Met Arg Tyr Glu Leu Gly Val Asp Ala Gly Tyr Thr Phe
             370                 375                 380

Thr Tyr Ser Glu Asp Gln Ala Leu Thr Pro Tyr Phe Lys Leu Ala Tyr
385                 390                 395                 400
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Val Tyr Asp Asp Ser Asn Asn Asp Asn Asp Val Asn Gly Asp Ser Ile
            405   410   415
Asp Asn Gly Thr Glu Gly Ser Ala Val Arg Val Gly Leu Gly Thr Gln
            420   425   430
Phe Ser Phe Thr Lys Asn Phe Ser Ala Tyr Thr Asp Ala Asn Tyr Leu
            435   440   445
Gly Gly Gly Asp Val Asp Gln Asp Trp Ser Ala Asn Val Gly Val Lys
            450   455   460
Tyr Thr Trp
465

    (210) 3??
    (211) 2??
    (212) PRT
    (213) E. Coli

    (400) ???

Met Pro Val Lys Asp Leu Thr Gly Ile Thr Ala Lys Asp Ala Gln Met
1   5   10   15
Leu Ser Val Val Lys Pro Leu Gln Glu Phe Gly Lys Leu Asp Lys Cys
            20   25   30
Leu Ser Arg Tyr Gly Thr Arg Phe Glu Phe Asn Asn Glu Lys Gln Val
            35   40   45
Ile Phe Ser Ser Asp Val Asn Asn Glu Asp Thr Phe Val Ile Leu Glu
            50   55   60
Gly Val Ile Ser Leu Arg Arg Glu Glu Asn Val Leu Ile Gly Ile Thr
61   70   75   80
Gln Ala Pro Tyr Ile Met Gly Leu Ala Asp Gly Leu Met Lys Asn Asp
                  85   90   95
Ile Pro Tyr Lys Leu Ile Ser Glu Gly Asn Cys Thr Gly Tyr His Leu
                  100   105   110
Pro Ala Lys Gln Thr Ile Thr Leu Ile Glu Gln Asn Gln Leu Trp Arg
            115   120   125
Asp Ala Phe Tyr Trp Leu Ala Trp Gln Asn Arg Ile Leu Glu Leu Arg
            130   135   140
Asp Val Gln Leu Ile Gly His Asn Ser Tyr Glu Gln Ile Arg Ala Thr
145   150   155   160
Leu Leu Ser Met Ile Asp Trp Asn Glu Glu Leu Arg Ser Arg Ile Gly
                  165   170   175
Val Met Asn Tyr Ile His Gln Arg Thr Arg Ile Ser Arg Ser Val Val
                  180   185   190
Ala Glu Val Leu Ala Ala Leu Arg Lys Gly Gly Tyr Ile Glu Met Asn
            195   200   205
Lys Gly Lys Leu Val Ala Ile Asn Arg Leu Pro Ser Glu Tyr
            210   215   220

    (210) ???
    (211) 64
    (212) PRT
    (213) E. Coli

    (400) 3??

Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys
1   5   10   15

Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro
        20   25   30

Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp
      35   40   45

Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys
     50   55   60

Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu
65   70   75   80

Lys Ala Val Leu

     <210> 1-4
     <211> 64
     <212> PRT
     <213> E. Coli

     <400> 1-4

Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
1   5   10   15

Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
        20   25   30

Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
        35   40   45

Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala
        50   55   60

     <210> 1-5
     <211> 1-6
     <212> PRT
     <213> E. Coli

     <400> 1-5

Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
1   5   10   15

Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
        20   25   30

Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
        35   40   45

Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
        50   55   60

Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
65   70   75   80

Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
            85   90   95

Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
          100   105   110

Ala Arg Glu Ala Phe Lys Leu Ala Ala Ala Lys Leu Pro Ile Lys Thr
          115   120   125

Thr Phe Val Thr Lys Thr Val Met
     130   135

     <210> 1-6
     <211> 135
     <212> PRT

<213> E. Coli

<400> 386

Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
1   5   10   15

Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
        20   25   30

Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
        35   40   45

Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
        50   55   60

Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
61   70   75   80

Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
                85   90   95

Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
            100   105   110

Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
            115   120   125

Met Pro Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
        130   135   140

Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
145   150   155   160

Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
                165   170   175

Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
            180   185   190

Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
            195   200   205

Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
210   215   220

Lys Lys Gln Gln Arg Lys Gly Arg Lys
225   230

<211> 3-7
<212> PRT
<213> E. Coli

<400> 3-7

Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys
1   5   10   15

Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala
        20   25   30

Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys
        35   40   45

Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala
        50   55   60

Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro
65   70   75   80

Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile
                85   90   95

Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg
            100   105   110

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<210> 788
<211> 92
<212> PRT
<213> E. Coli

<400> 788

Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu
1   5   10   15
Met Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg
            20   25   30
Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr
        35   40   45
Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp
        50   55   60
Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr
65   70   75   80
Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys
                85   90

<210> 789
<211> 223
<212> PRT
<213> E. Coli

<400> 789

Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val
1   5   10   15
Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro
                20   25   30
Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg
        35   40   45
Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile
        50   55   60
Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg
65   70   75   80
Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr
                85   90   95
Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala
            100   105   110
Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn
            115   120   125
Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val
        130   135   140
Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr
145   150   155   160
Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
                165   170   175
Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
            180   185   190
Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
            195   200   205
Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala
        210   215   220

Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe
225   230   235   240
Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys
                245   250   255
Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser
                260   265   270
Lys

<210> 3..
<211> ...
<212> PRT
<213> E. Coli

<400> 14

Met Ile Arg ... Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val
1   5   10   15
Ser Gly Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu
                20   25   30
Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln
                35   40   45
Lys Leu Phe ... Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys
                50   55   60
Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp
65   70   75   80
Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val
                85   90   95
Gly Gly Ala Glu
                100

<210> ...
<211> ...
<212> PRT
<213> E. Coli

<400> 15

Met Gln Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
1   5   10   15
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
                20   25   30
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
                35   40   45
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
50   55   60
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser
65   70   75   80
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val
                85   90   95
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu
                100   105   110
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala
                115   120   125
Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu

```
        130                    135                        140
Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala
145                    150                    155                    160
Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp
                         165                    170                    175
Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
                         180                    185                    190
Val Lys Gln Val Glu Glu Met Leu Ala
                         195                    200
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<210> 392
<211> 205
<212> PRT
<213> E. Coli

<400> 392

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Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
1                    5                    10                    15
Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
                    20                   25                   30
Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
                    35                   40                   45
Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
                    50                   55                   60
Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
65                   70                   75                   80
Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
                    85                   90                   95
Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
                    100                  105                  110
Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
                    115                  120                  125
Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
                    130                  135                  140
Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
145                  150                  155                  160
Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp
                    165                  170                  175
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala
                    180                  185                  190
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys
                    195                  200                  205
Ala
```

<210> 393
<211> 103
<212> PRT
<213> E. Coli

<400> 393

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Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
1                    5                    10                   15
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Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
                20   25   30
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
          35   40   45
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
      50   55   60
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
65   70   75   80
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
                85   90   95
Asp Val Gln Ile Ser Leu Gly
                100

<210> 344
<211> 118
<212> PRT
<213> E. Coli

<400> 344
Met Ala Arg Val Lys Arg Gly Val Ile Ala Arg Ala Arg His Lys Lys
1   5   10   15
Ile Leu Lys Gln Ala Lys Gly Tyr Tyr Gly Ala Arg Ser Arg Val Tyr
          20   25   30
Arg Val Ala Phe Gln Ala Val Ile Lys Ala Gly Gln Tyr Ala Tyr Arg
          35   40   45
Asp Arg Arg Gln Arg Lys Arg Gln Phe Arg Gln Leu Trp Ile Ala Arg
      50   55   60
Ile Asn Ala Ala Ala Arg Gln Asn Gly Ile Ser Tyr Ser Lys Phe Ile
65   70   75   80
Asn Gly Leu Lys Lys Ala Ser Val Glu Ile Asp Arg Lys Ile Leu Ala
                85   90   95
Asp Ile Ala Val Phe Asp Lys Val Ala Phe Thr Ala Leu Val Glu Lys
                100   105   110
Ala Lys Ala Ala Leu Ala
          115

<210> 345
<211> 65
<212> PRT
<213> E. Coli

<400> 345
Met Pro Lys Ile Lys Thr Val Arg Gly Ala Ala Lys Arg Phe Lys Lys
1   5   10   15
Thr Gly Lys Gly Gly Phe Lys His Lys His Ala Asn Leu Arg His Ile
          20   25   30
Leu Thr Lys Lys Ala Thr Lys Arg Lys Arg His Leu Arg Pro Lys Ala
          35   40   45
Met Val Ser Lys Gly Asp Leu Gly Leu Val Ile Ala Cys Leu Pro Tyr
    50   55   60
Ala
65

<210> 396
<211> 180
<212> PRT
<213> E. Coli

<400> 396

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Met Lys Gly Gly Lys Arg Val Gln Thr Ala Arg Pro Asn Arg Ile Asn
1               5                   10                  15
Gly Glu Ile Arg Ala Gln Glu Val Arg Leu Thr Gly Leu Glu Gly Glu
            20                  25                  30
Gln Leu Gly Ile Val Ser Leu Arg Glu Ala Leu Glu Lys Ala Glu Glu
        35                  40                  45
Ala Gly Val Asp Leu Val Glu Ile Ser Pro Asn Ala Glu Pro Pro Val
        50                  55                  60
Cys Arg Ile Met Asp Tyr Gly Lys Phe Leu Tyr Glu Lys Ser Lys Ser
65                  70                  75                  80
Ser Lys Glu Gln Lys Lys Lys Gln Lys Val Ile Gln Val Lys Glu Ile
                85                  90                  95
Lys Phe Arg Pro Gly Thr Asp Glu Gly Asp Tyr Gln Val Lys Leu Arg
                100                 105                 110
Ser Leu Ile Arg Phe Leu Glu Glu Gly Asp Lys Ala Lys Ile Thr Leu
            115                 120                 125
Arg Phe Arg Gly Arg Glu Met Ala His Gln Gln Ile Gly Met Glu Val
            130                 135                 140
Leu Asn Arg Val Lys Asp Asp Leu Gln Glu Leu Ala Val Val Glu Ser
145                 150                 155                 160
Phe Pro Thr Lys Ile Glu Gly Arg Gln Met Ile Met Val Leu Ala Pro
                165                 170                 175
Lys Lys Lys Gln
                180
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<210> 397
<211> 641
<212> PRT
<213> E. Coli

<400> 397

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Met Pro Val Ile Thr Leu Pro Asp Gly Ser Gln Arg His Tyr Asp His
1               5                   10                  15
Ala Val Ser Pro Met Asp Val Ala Leu Asp Ile Gly Pro Gly Leu Ala
            20                  25                  30
Lys Ala Cys Ile Ala Gly Arg Val Asn Gly Glu Leu Val Asp Ala Cys
        35                  40                  45
Asp Leu Ile Glu Asn Asp Ala Gln Leu Ser Ile Ile Thr Ala Lys Asp
        50                  55                  60
Glu Glu Gly Leu Glu Ile Ile Arg His Ser Cys Ala His Leu Leu Gly
65                  70                  75                  80
His Ala Ile Lys Gln Leu Trp Pro His Thr Lys Met Ala Ile Gly Pro
                85                  90                  95
Val Ile Asp Asn Gly Phe Tyr Tyr Asp Val Asp Leu Asp Arg Thr Leu
                100                 105                 110
Thr Gln Glu Asp Val Glu Ala Leu Glu Lys Arg Met His Glu Leu Ala
            115                 120                 125
Glu Lys Asn Tyr Asp Val Ile Lys Lys Lys Val Ser Trp His Glu Ala
```

```
                130                  135                    140
Arg Glu Thr Phe Ala Asn Arg Gly Glu Ser Tyr Lys Val Ser Ile Leu
145                  150                  155                  160
Asp Glu Asn Ile Ala His Asp Asp Lys Pro Gly Leu Tyr Phe His Glu
                    165                  170                  175
Glu Tyr Val Asp Met Cys Arg Gly Pro His Val Pro Asn Met Arg Phe
                180                  185                    190
Cys His His Phe Lys Leu Met Lys Thr Ala Gly Ala Tyr Trp Arg Gly
                195                  200                    205
Asp Ser Asn Asn Lys Met Leu Gln Arg Ile Tyr Gly Thr Ala Trp Ala
        210                  215                    220
Asp Lys Lys Ala Leu Asn Ala Tyr Leu Gln Arg Leu Glu Glu Ala Ala
225                  230                    235                  240
Lys Arg Asp His Arg Lys Ile Gly Lys Gln Leu Asp Leu Tyr His Met
                    245                  250                  255
Gln Glu Glu Ala Pro Gly Met Val Phe Trp His Asn Asp Gly Trp Thr
                260                  265                    270
Ile Phe Arg Glu Leu Glu Val Phe Val Arg Ser Lys Leu Lys Glu Tyr
                275                  280                    285
Gln Tyr Gln Glu Val Lys Gly Pro Phe Met Met Asp Arg Val Leu Trp
        290                  295                    300
Glu Lys Thr Gly His Trp Asp Asn Tyr Lys Asp Ala Met Phe Thr Thr
305                  310                  315                  320
Ser Ser Glu Asn Arg Glu Tyr Cys Ile Lys Pro Met Asn Cys Pro Gly
                    325                  330                  335
His Val Gln Ile Phe Asn Gln Gly Leu Lys Ser Tyr Arg Asp Leu Pro
                340                  345                    350
Leu Arg Met Ala Glu Phe Gly Ser Cys His Arg Asn Glu Pro Ser Gly
                355                  360                    365
Ser Leu His Gly Leu Met Arg Val Arg Gly Phe Thr Gln Asp Asp Ala
        370                  375                    380
His Ile Phe Cys Thr Glu Glu Gln Ile Arg Asp Glu Val Asn Gly Cys
385                  390                  395                  400
Ile Arg Leu Val Tyr Asp Met Tyr Ser Thr Phe Gly Phe Glu Lys Ile
                    405                  410                  415
Val Val Lys Leu Ser Thr Arg Pro Glu Lys Arg Ile Gly Ser Asp Glu
                420                  425                    430
Met Trp Asp Arg Ala Glu Ala Asp Leu Ala Val Ala Leu Glu Glu Asn
                435                  440                    445
Asn Ile Pro Phe Glu Tyr Gln Leu Gly Glu Gly Ala Phe Tyr Gly Pro
        450                  455                    460
Lys Ile Glu Phe Thr Leu Tyr Asp Cys Leu Asp Arg Ala Trp Gln Cys
465                  470                  475                  480
Gly Thr Val Gln Leu Asp Phe Ser Leu Pro Ser Arg Leu Ser Ala Ser
                    485                  490                  495
Tyr Val Gly Glu Asp Asn Glu Arg Lys Val Pro Val Met Ile His Arg
                500                  505                    510
Ala Ile Leu Gly Ser Met Glu Arg Phe Ile Gly Ile Leu Thr Glu Glu
                515                  520                    525
Phe Ala Gly Phe Phe Pro Thr Trp Leu Ala Pro Val Gln Val Val Ile
        530                  535                    540
Met Asn Ile Thr Asp Ser Gln Ser Glu Tyr Val Asn Glu Leu Thr Gln
545                  550                  555                  560
Lys Leu Ser Asn Ala Gly Ile Arg Val Lys Ala Asp Leu Arg Asn Glu
                    565                  570                  575
Lys Ile Gly Phe Lys Ile Arg Glu His Thr Leu Arg Arg Val Pro Tyr
                580                  585                    590
```

Met Leu Val Cys Gly Asp Lys Glu Val Glu Ser Gly Lys Val Ala Val
        535   500   505

Arg Thr Arg Arg Gly Lys Asp Leu Gly Ser Met Asp Val Asn Glu Val
    610   615   620

Ile Gln Lys Leu Gln Gln Glu Ile Arg Ser Arg Ser Leu Lys Gln Leu
625   630   635   640

Glu Glu

    (210) 238
    (211) 465
    (212) PRT
    (213) E. Coli

    (400) 98
Met Thr Lys His Tyr Asp Tyr Ile Ala Ile Gly Gly Gly Ser Gly Gly
1   5   10   15

Ile Ala Ser Ile Asn Arg Ala Ala Met Tyr Gly Gln Lys Cys Ala Leu
        20   25   30

Ile Gln Ala Lys Glu Leu Gly Gly Thr Cys Val Asn Val Gly Cys Val
        35   40   45

Pro Lys Lys Val Met Trp His Ala Ala Gln Ile Arg Glu Ala Ile His
    50   55   60

Met Tyr Gly Pro Asp Tyr Gly Phe Asp Thr Thr Ile Asn Lys Phe Asn
65   70   75   80

Trp Glu Thr Leu Ile Ala Ser Arg Thr Ala Tyr Ile Asp Arg Ile His
            85   90   95

Thr Ser Tyr Glu Asn Val Leu Gly Lys Asn Asn Val Asp Val Ile Lys
            100   105   110

Gly Phe Ala Arg Phe Val Asp Ala Lys Thr Leu Glu Val Asn Gly Glu
        115   120   125

Thr Ile Thr Ala Asp His Ile Leu Ile Ala Thr Gly Gly Arg Pro Ser
        130   135   140

His Pro Asp Ile Pro Gly Val Glu Tyr Gly Ile Asp Ser Asp Gly Phe
145   150   155   160

Phe Ala Leu Pro Ala Leu Pro Glu Arg Val Ala Val Val Gly Ala Gly
                165   170   175

Tyr Ile Ala Val Glu Leu Ala Gly Val Ile Asn Gly Leu Gly Ala Lys
                180   185   190

Thr His Leu Phe Val Arg Lys His Ala Pro Leu Arg Ser Phe Asp Pro
        195   200   205

Met Ile Ser Glu Thr Leu Val Glu Val Met Asn Ala Glu Gly Pro Gln
    210   215   220

Leu His Thr Asn Ala Ile Pro Lys Ala Val Val Lys Asn Thr Asp Gly
225   231   235   240

Ser Leu Thr Leu Glu Leu Glu Asp Gly Arg Ser Glu Thr Val Asp Cys
                245   250   255

Leu Ile Trp Ala Ile Gly Arg Glu Pro Ala Asn Asp Asn Ile Asn Leu
            260   265   270

Glu Ala Ala Gly Val Lys Thr Asn Glu Lys Gly Tyr Ile Val Val Asp
    275   280   285

Lys Tyr Gln Asn Thr Asn Ile Glu Gly Ile Tyr Ala Val Gly Asp Asn
    290   295   300

Thr Gly Ala Val Glu Leu Thr Pro Val Ala Val Ala Ala Gly Arg Arg
315   311   315   320

Leu Ser Glu Arg Leu Phe Asn Asn Lys Pro Asp Glu His Leu Asp Tyr

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            325                 330                 335
Ser Asn Ile Pro Thr Val Val Phe Ser His Pro Pro Ile Gly Thr Val
            340                 345                 350
Gly Leu Thr Glu Pro Gln Ala Arg Glu Gln Tyr Gly Asp Asp Gln Val
            355                 360                 365
Lys Val Tyr Lys Ser Ser Phe Thr Ala Met Tyr Thr Ala Val Thr Thr
            370                 375                 380
His Arg Gln Pro Cys Arg Met Lys Leu Val Cys Val Gly Ser Glu Glu
385                 390                 395                 400
Lys Ile Val Gly Ile His Gly Ile Gly Phe Gly Met Asp Glu Met Leu
                    405                 410                 415
Gln Gly Phe Ala Val Ala Leu Lys Met Gly Ala Thr Lys Lys Asp Phe
                    420                 425                 430
Asp Asn Thr Val Ala Ile His Pro Thr Ala Ala Glu Glu Phe Val Thr
                    435                 440                 445
Met Arg
        450
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    <210> 143
    <211> 1894
    <212> RNA
    <213> E. Coli

    <400> 399
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aaggiauagc cicacguuc auuauaccg uuuagcucaa cgcaucgcug cgcuuacaca        60
ccgggcaug caacgugcag gucuucug uaccuccu accaaucaa gggcaggag       120
aacuacuuc ggggaagug ucgucgcau augcuucag cacucauc uuccgcauu       180
agoucgg cagucgacu ggcaugaca cccgaacac agucgaugcc ccaccgauu       240
ccucucui agggcgaga cccuucaui ucuccagcgc ccaggcagag uaggqaccga    300
acguauci gagguuucaa acccagucg cguaccacui aaaaggaga agagccauac    360
ccugggaugo uacucagcc ccaggaugug augagcgac aucgaggugc caaacacgc    420
cgucgauigc aacucucugg cggiaucgcc cuguuaiucc cggaguaccu uucuaicgau  480
gagcgauugc ccuuccauuc agaacacacg gaucacuaug accigcccc ggaccugcuc  540
gggcgucau gcucggcagu aagcuggcuu aiggccaucc aciaaccicc ugauguccga   600
ccaggauuu caaccuucu uguuccicg uuaaucuuu ggaggagacc gcccccaguca    660
aacuacuac cagacacgu ccgcuaccg uauuacggu caacguuaga acaucaaaca     720
uuaaaguuu guauucaag guggccucca ucgagacug cguccacaci uaaaagcuc    780
ccaccucau uacacaucaa gggicuaagu ucagugicac gcuauaguaa aggiuucagg    840
ggucuuug ucuugcgcg gguauacgc aucucacag cgaguuaau uuacugagu        900
cucgggiiga gacagccigg ccaiucacuc gccaiucgig caggucggaa cuuaccigac    960
aaggaauuc gciacciuag gacggiaia guuacggcug ccuucuacci gggcuuigau    1020
caagaguuuc gcugcgicaa accccaicaa uuaacciucc ggcacgcgg aggcgucaca     1080
acgiuauigu ccaiuucugu guuugcacag ugcugucuru uaaauaaaca guugcagca     1140
gciggiaici ucgacigaui ucaguicau cccgcgaggga ccucaccuuc auaucaguu    1200
gccuccuccc gaauucacgg caccaiuiui ccuaguucci uacccgagu ucucucaaic    1260
ggccuguau ucucuaccuu accaccgiug ucgggaiiggg guaggaiuug auguiacug     1320
auguuagai gcuucuccug gaagcaggc auuguuigci ucagcacgci agigcciegu     1380
caccacicci cagccuugau uuicggaiui ugccuggaaa accagccuac aggcuuaaac    1440
cgggacuacc guggccgggc caacauagcc uicuccgucc cccuuugca guaacaccaa    1500
guacaguaui auuaaccugu uuccaucga cuaccgciui uggocuugcc uuagggguig    1560
acuacuiug cccgaiuaa cguiggacag gaaaccuigg ucuuccggcg aggggicuu     1620
ucaccciuu uaucguiacu uaugucaca uuggcacuic ugaaccuicc agcaugccuc    1680
acagcaucci uucgicaggcu uacagaacgc ucicccuaccc aacaaacgau aaggcucgcu   1740
gcgcgagiuu cggigcaugg uuuagccicg uuacaucuic cgcgcagocc gacucgacca    1800
gugagciauu acgcuuucuu uaaaugaugg cugcuicuaa gccaacaucc uggcuguicug   1860
```

ggccguuccca cauuguuugc cacuuaacca ugacuuuggg accuucagcug gcgggcuggg   1900
ucuguuuucca cuucacgagc gacguugaca cucgccgucg gucucucgcg auaacauuu   1960
ccgggcauuuc cacuuucacu cggguuggca agucgggcau acccccuugc cgaaacaguu   2040
cucuccucgg ... gccuaccaaau agcuucgugg gagaaccagc   2100
...
aagcugga ... augggcuagau   2040
cacggguuu ... guucccccua   2040
ggcccauuc ... auacaaaag   2040
ucuacgauc ... uucaggucu   2400
cuuccacuc ... uucaccaua   2440
gucaguccag ... ggcauaccag   2500
ccacccuuca ... ggcgucgggcuu   2040
ccacacuc ... gcucagggcu   2040
gcuccccca ... cucgggguac   2700
uuagugucu ... aaguguaguu   2740
ugucgaaca ... ucauuuccacc   2040
uuuaccguuge ... agggcaucca   2040
ccgguuugu ... uc   2004

<210> 4..
<211> 1..
<212> RNA
<213> E. Coli

<400> 4.
augccuguaa cuuccuacu cucggcauggg gagaccccac acuaccaucg gcggcuacggc   ..
guuucaacuc ugaucuuggc auggggucag guggggaccac cggcgcuaggg ccggcaggca   1..

<210> 4.1
<211> ..
<212> RNA
<213> E. Coli

<400> 4.1
uagcccuuucg uuuggagggc caggacacgg ccccuucacg ggcgguaacag gggguucgaau   ..
ccccauugg aguaa   ..

<210> 4..
<211> 1549
<212> RNA
<213> E. Coli

<400> 4..
aaauuguagag guuugucacu uccucuaggc uggcucagauu uaaugccuuc ggcaggccuc acacaugaaa   ..
uccgaauugu aacugggaca ucgcuugcac uuccugugac aggggggcag gggguggauaa   1..
ugucuugucaa gcuucccgac ggggggggg uuu aacuacugga aacgggucguu aaauaccgcau   1..
aaaguccuaa gac aaaagau ggggaccucc ggccccucuu ccaugggaug ugccacgaug   2.1
ggauuaguuu guuuguggg uaacgggcaca ccaaggcgac gauccccagc uggucugaga   ...
ggaugaccag ccacacugga acugagacac ggucccagac ccuacgggag gcagcagugg   500
ggaauauugcu caaaugggcg caaagccugac ggcagccacg ccgcguguga aagaaggccu   4..
ucggguuguuaa aaguacuuu agcggggggg aagggaguaaa aguuaauacc uuuugcucauu   450

gaccuuaccc gcugaagaag caccggcuaa cuccgugcca gcagccgcgg uaauacggag   540
gucaauacgg uuaucuuugg uuaacuggcg uaaagcgcac gcaggcgggu ugguuaaguc   600
agauguguaa ucccgcggcu caaccucgga acugcaucua auacuggcaa gcugaguucu   660
canaccuagg guagaauucc caggugcagc ggugaaaugc guagagaucu ggaggaauac   700
cggugguugc gaaggcgacu gggcuggaac agugcacgaa aggcgaagca gcaccaggug   750
gcaacaggau uagauaccuc guaguccacg ccguaaacgc uguugacuag gagguugcac   810
ccaccugggc uguucaacuu cagucggggg ugccgacaag cggugggagc augggguuaa   870
aauucgaugc aacgcgaaga accuuacccu ggucuugaca ucagagauga ucaucuuuaa   960
uuacucagag ucgcgaagaa acggaaacgg gggaaacgcc aggaccgaaa caggcgguca   1020
uaauugugug uc [illegible]   1080
aaaguuuugg uuaagucuc ccaagagcgc aaccccuauc ccuuguaagc aggggucaagu   1140
ccguuaacu aaaguuagua gccaaugaua aacaggagga agguggggau gacguaaagu   1200
caucauggcc cuuacgaccu gggcuacaca cgugcuacaa uggcgcauac aaagagaagc   1260
gaccucugcu gaaagcuggc accuauaaau uugcguccuc gucuggauug gaguucugaa   1320
gcaaagccac ugaguccggg auccucguac aucgugggcu caagaaugca ggugaauacg   1380
uucccuggcc uuguacacac cgcccgucac accauggggg uugggucugc aagaaguagg   1440
uagucuaacc uucggggagg cucuaccacu uugugauuc augacugggg ugaagucguu   1500
acaagguaac cguaggggaa ccugcgguug gaucaccuuc uuaccuaa   1549

<210> 403
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer Oligonucleotide

<400> 403
tgtttatcaa aacctt   17

<210> 404
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer Oligonucleotide

<400> 404
acaatttaac acacctc   17

<210> 405
<211> 157
<212> DNA
<213> Escherichia coli

<400> 405
caggtggtat cgaaacccaa aatggagacg ggaagctgaa ccagatagtt actggaggtg   60
atcaccagca gatcaaataa cgataaccag aacaacgcct tatagcgttg agtttgcgag   120
aaaacgttca tatgtacct ttttgattaa ccattgggg   153

<210> 406
<211> 640
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(640)
<223> n = A,T,C or G

<400> 406

nggnncaaa gtgtttgggn cgggcaactg gaggccaacc ttaanttngg ggaaattttt   60
aanaaaaggc ggggatttgt nagccacggg ngattanttt anaataaatt aagtgttgcc   120
ataaiggggac aaagngaagg aagtggntat taanggannc gccaatgcga nttagggcag   180
accattcggc cattcgtcctt cttggttatc gaagttcatc cagatagccg ttgccngacc   240
cacacagattc ggttcnggca caaagcccca gtaacggctg tccgcgctgt tgtcgcggtt   300
gtcgccatc atgaagtatt gtcccggagg aacaatcccag gttgccagtt gttgcctgg   360
ctgttggtaa tacatcccca cctgatcctg cggcaatcggc actgtcagaa tcggtgcgt   420
caaatcaccc agtgtctctt tacgctcgga aagacgaatt ccatttctt tggtttcgtt   480
tttcgccact tcaaagaatc cgctggtcgc ttcccccacca ttacggcgtg agaaggtctg   540
aacaaaatcg ctcggttcca cgtttgagta ggtgaccggc agcgcgtttt cacacgcctg   600
tcccggaactg catcccggtt gaaacgtcag ctctttttgag   640

<211> 407
<211> 632
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(632)
<223> n = A,T,C or G

<400> 407

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tcccattcggc aggacaact tcggttaaag tcgcaaatatt atcatctgca cttcactcgt   120
cagctaaggcg gatggagtgg ccggaaaacct catagtgacc gcccaccagt tggcctgcat   180
ncgtttcgtag cgtacgcgcg gcattcggcaa taagattcag atactcagac tcttccgggg   240
ncti tgccag cataaaagag gaggatgctc cggtatccag caactgctcc aggcaaatt   300
gcagccgcgg ttgagtatca ctgaataaag gatcgtttc gtcaatcaaa tgttggctgag   360
caaatatttc ctgatagcta tcggtatcag gaaccaggtc acgccatgca agtttcgtaa   420
tggtcaaagt tgatgtcttt tagtctgttg tcaaagccgc nattatatccn gtaaccggca   480
ctatcgtaaca cgtagaaagc acccgacaat actcctggca tgggcgttaa agtccacagg   540
atgccgatct ttccttcact ggcctaaaaa gctgatattc tgtaaagagt tacacngtaa   600
tattcagatc gctatgaaat atcaacaact tggaaaatct tgnaaagcng gttggaaaat   660
ctaaagtatc tggttaagaa gc   682

<211> 408
<211> 309
<212> DNA
<213> Escherichia coli

<400> 408

ggggatcggg cagaatttta cgctgaccaa tgacgcgacg acgtggcatg gaaatactcc   60
gttgttaatt caggattgtc caaaactcta cgagtttagt ttgacattta agttaaaacg   120
ttttcgctta cttaacggag aaccattaag cgttaggacg cttcacgcca tacttggaac   180
gagccgtgctt acggtctttta acgccggagc agtcaagcgc accacgtacg gtgtggtaac   240
caaacccggg gaggtcttta acacgacgc cacggatcag gatcacggag tgctcctgca   300
gtccagctt   309

<211> 409
<211> 1167

<211> DNA
<213> Escherichia coli

<400> 409
gtcracccat ctgtccattg agcggacagt ttgtgcaaca ctattttgtt gaccggaaaa   60
tggacaltt tccgcaatgc ctgttgctat cacgcttaaa ccatttcatt gggatttaca   120
cagaacaac gtcctgtgc agtatattaa gtcgtcgata gaaacaagca ttgaaaggca   180
cagagtatt caaacagtgt gaaagctac tggcgcctta cagcgcaaaa aggctggtga   240
ctaaaaatc agcagcac agcctgattt ctaggctgc aaccggaagg gttggcttat   300
ttaattcaa cttcagcgc agcttcttcc agagctttt tcagtgcttc tgcgtcgtct   360
ttgtcacgc cttctttcag agcagccggt ggagattcta ccaggtcttt agcttcttc   420
agaccaatcc cagttgcgcc agtactgct ttgataacag caactttgtt agcgccagca   480
gctttagaa ttagtcggaa ttcagtcttt tcttcagcag cttcaaccgg gccagcagct   540
ctatctcag cagcagcagc ggaaacaccg aatttttctt ycattgcaga gatcaagttc   600
tataacgtcc attacagaca tagctgcaac tgcttcaatg awttgatctt tagtgataga   660
catttaaatk gttcctgaat atcagaataa gtttatacgt aagcgaatgc gttaaaaaja   720
taattgcgaw taagcagctt ytttcgcatc gcgtacagma gccagagtac gaaccagttc   780
tcccgcgaa gcttctttca tcgttgccat caggcgtgca attgcttctt cgtaggtcgg   840
cagtgtttcc aggcggtcga tctgagacgc cgggatcagc tcacctcaa aggcagcggc   900
tttacctca aattttgcat tcgctttcgc gaactctttg aacagacgag cagcagcgcc   960
cgcttgtttcc atagagtatg caatcaggt cggaccaaca aacgcgtctt tcaggcactc   1020
taattggagta ccttcaacag caacggcgcag caaggtgtta cgaacaacac gcatgtatac   1080
gncagcttcg cgaacctgctt taacgcagttc agtcatttta tctacagtta cgcccacggg   1140
gattggcgac tactgcaage caagctt   1167

<211> 413
<211> 4 4
<211> DNA
<213> Escherichia coli

<400> 411
caacgcatt ttgktggacc ggaaaakgga acacttccg cawkgcctgt tgctatcacg   60
gttaaacat tccattgcgg tttacacaga agggacgtcc tgtgcgagta tattaagtcg   120
tcgatagaa caagcattga aaggcacagc agtagtcaaa cagtgtgaaa cgctactggc   180
gccttacgc ggaaaaaggc tggtgactaa aaagtcacca gccatcagcc tgatttctca   240
ggctgaacc ggaaggggttg gcttatttaa cttcaacttc agcgccagct tcttccagag   300
ctttttcag tgcttctgcg tgtctttgtc tcaagctttc tttcagagca gccggtgcag   360
atcctaccag gtctttagct tctttcagac ccaggccagt tgcg   404

<210> 411
<211> 152
<212> DNA
<213> Escherichia coli

<400> 411
aghachttt tcaagtgcttc tgcgtcgtct ttgctcacgc cttcttttcaa gagcagccg   60
ctgagattc taccaggtctt ttagcttctt tcagacccag gccagttgcg ccacgtactg   120
cttttaataac agcaactttg ttagcgccag ca   152

<210> 411
<211> 411
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(325)

<223> n = A,T,C or G

<400> 412

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gatcgtcga cccatctgtc cattgagcgg acagtttgtg caacactatt ttgttgaccg      60
gaaaatggaa cactttccgc aatgcctgtt gctatcacgc ttaaaccatt tcattgcgat     120
ttaacagaa cggacgtcct gtggcagtat attaagtcgt cgatagaaac aagcattgaa      180
aggcacagta gtagtcaaac agtgtgaaac gctactggcg ccttacagcg caaaaaggct     240
gttgactaaa aagtcaccag ccatcagcct gatttctcag gctgcaaccg gaagggttgg     300
cttattaac tccaacttca gcgccagct cttccagagc tttttcagt gcttctgcgt        360
cgtcttgct cacgccttct ttcagagcag ccgggtgcag attctaccag gtctttagct      420
tcttttcagac ccaggccagt tgcgccagt actgctttga taacagcaac tttgttagcg     480
ccagcagctt tcagaattac gtcgaattca agtttttct tcagcagctt caaccgggcc      540
atcagctaca gctacagcag cagcagcgga aacacgaat ttttcttgca ttggcagaga      600
tcaagtctca caacgtccat tacagacata gctgcaactg cttcaatgat tcgatccttwa    660
ggcacagaca tttaaattgt tcctgaatat cagaataagt ttatacgtaa ggcaatcgct     720
ttaaaagata actcgcatta agcagtcct ttcgcatcgc gtacagcage cagaggtcga      780
cccagtttgc cagccgaagg ttggcttttc agcctnnncn natta                     825
```

<210> 413
<211> 428
<212> DNA
<213> Escherichia coli

<400> 413

```
attattcaaa caggtgkgca aagctactgg cggcttacag cgcaaaaagg ctggtgacta      60
aaaagtcacc agccatcagc ctgatttctc aggctgcaac cggaaggg tggcttatt        120
atttaaat tccagcgcag cttcttccag agctttttc agtgcttctg cgtcgtcttt        180
gctcacgcc tcttttcagag cagccgggtgc agattctacc aggtctttag cttcttttcag    240
atttagcatt gttgcgccac gtactgcttt gataacagca actttgttag cgccagcagc      300
tttcagaatt acgtcgaatt cagtttttt tccagcagct tcaacgggc cagcagctac       360
agctacagca gcagcaggga aaacacccga attttttctc cattgcagag atcaagtcct      420
gtaaat                                                                 427
```

<210> 414
<211> 126
<212> DNA
<213> Escherichia coli

<400> 414

```
ttagtttttt tccagtgctt cgggtcgtct ttgctcaggc cttctttcag agcagccggt      60
ttagatttta ccaggtcttt agcttctttc agagccaggc cagtgcgcc agtactgct       120
ttgata                                                                 126
```

<210> 415
<211> 264
<212> DNA
<213> Escherichia coli

<400> 415

```
ctgcaaccg gatgggttgg cttatttaac tccaacttca gcgccagctt cttccagagc      60
tttttcag tgcttctgcg tcgtctttgc tcacgcctc tttcagagca gccgggtgcag       120
attttacag gtctttagct tcttttcagac ccaggccagt tgcgccagt actgctttga      180
taacagcaac tttgttagcg ccagcagctt tcagaattac gtcgaattca gttttttctt     240
tagcagcttc aacgggcca gcag                                             264
```

<210> 416
<211> 201
```

<210> DNA
<213> Escherichia coli

<400> 416
cgcatacct gcagcatcgg ccgatggag atcaggtcgg cagaacgctg taccgctttg   60
taggtgtgt taccggtgtt cagatccggg aagatgaaca cggtagcgcg acctgcaacc   120
gaacgttcg gcgctttgga tttgcaacg tcagccatta ccgcagcgtc gtactgcagc   180
gaacgtcga tcatcaggtc a   201

<210> 417
<211> 239
<212> DNA
<213> Escherichia coli

<400> 417
aattcagtag ttgacagtgg cataaacgta actggtgact tttgcccggc atgacgcgg   60
gctttttta ttattccgtg acttccagcg tagtgaaggc aaacttctcg ccatcaaata   120
gcccatgact ggttagtttt agcgcggggga tcactggcag agaaagaaac gccatctgaa   180
taagggcgc atggggtaac ggacogcatt caogggcggc ggctttcaag gcgtcaatt   240

<210> 418
<211> 233
<212> DNA
<213> Escherichia coli

<400> 418
ttctttttt cgtcaacggt gtccagaatc attttattta cctcgggtac ttatgctgat   60
ttttattatt atggggaagg tgttatttat gagtttcatt tatgccgtaa cgacaatgaa   120
ctccggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt   180
aatactattt aaatatttatt ttgagccatat gaacataagg ttg   223

<210> 419
<211> 223
<212> DNA
<213> Escherichia coli

<400> 419
ttctttttt cgtcaacggt gtccagaatc attttattta cctcgggtac ttatgctgat   60
tttattatt atggggaagg tgttatttat gagtttcatt tatgccgtaa cgacaatgaa   120
ctccggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt   180
aatactattt aaatatttatt ttgagccatat gaacataagg ttg   223

<210> 420
<211> 212
<212> DNA
<213> Escherichia coli

<400> 420
aatacgcggt atgcacgcct ttctttttt cgtcaacggt gtccagaatc attttattta   60
tctcgggtac ttatgctgat tttattatt atggggaagg tgttatttat gagtttcatt   120
tatgccgtaa cgacaatgaa ctccggaatt agtataagca gcgcgagaat aataatcatt   180
gtgcaaatgc taatttaatt aatactattt aa   212

<210> 421
<211> 348
<212> DNA
<213> Escherichia coli

<210> 421

<400> 421
```
cgctataaat tatcgcgcgt ggcataaaaa ctggctccaa acgccgtctt tgccagcagc      60
cagggcataa atgcaccag aattatcgtc aagcaaccaa ttgctgaaac gccaagcagc     120
aggcgggtgg agagctgttt cagttcggcg ggtaaccctt caatccattt gccgccagtc     180
cacacaaca tgatgccccc gtacaaccc aacgtgccaa gggtggcaac aatggcaggg     240
atcttagcc acggcgaca gacacgttg aaaaatcccg cgagcaaac aagcagaaa     300
gtgcgacac aagcaacagg tagtgaatat cctcgttca gtaacatccc caacagcacc     360
ggcgcattc cgggtaatcg aaccccactt gaaacatcaa tattggcgt aagcattwcc     400
aagcttcgs gcccatkg                                                    418
```

<210> 422
<211> 642
<212> DNA
<213> Escherichia coli

<400> 422
```
acttccgtg gatccgtcga ccgtgcgctt ccggttgtgg caacccgcga aatggcgcgg      60
ccgtaagtct gggggggtta ttccttcccc gttgaggaca ccgggttgtc aggttgacca     120
taccgcttag tgacaacccc ggtgcaacgc cctctgttat caatttctg gtgacgtttg     180
cgggatag tcttactcg tgactgctct gccgcccctt ttaaagtgaa ttttgtgatg     240
tgtaaatc ggtgagcgc acgcggaaca gttaaaacca aaaacagtgt tatgggtgga     300
ttctctat ccggcgttaa ctgttaactg gctaacgtca cctggaggca ccaggcactg     360
cacacaca tccattgttg aggacgcgac aatgaaaacg ttattaccaa acgtaaatac     420
gtctaaatct tgttttgaaa ttggtgtcac tatcagtaac ccagtattta ctgaagatgc     480
cattaataag agaaaacaag aacgggagc attaaataaa atatgcattg tttcaatgct     540
gtctcgttta cgtctgatc caaaaggatg ttgcacaatga attcagcact tgtgcttgtt     600
ctgacagttt ttctgtttc cggagagcca gttgatattg cagtcagtgt tcacaggaca     660
atggcgggt gatgactgaa gc                                                642
```

<210> 423
<211> 600
<212> DNA
<213> Escherichia coli

<400> 423
```
gcggttcaa tcgtgactgc tctgccgccc ttttaaagt ggaatttgtg atgtggtgaa      60
tcggtctaag cgcacgcgga acagttaaaa ccaaaaacag tgttatgggt ggattctctg     120
tatccgggat taatcgttaa ctggttaacg tcacctggag gcaccaggca ctgatcacca     180
aaatcatg ttgaggaccg gataatgaaa acgttattac caaacgttaa tacgtctgaa     240
ggtgatttg aaatcgggtc cactatcagt aacccagtat ttactgaaga tgccattaac     300
agataaaac aagaacggga gctattaaat aaaatatgca ttgtttaat ggtggtcgt     360
ttacgtctat a tgccaaaag atgtgcacaa tgaattcagc atttgtgct gttctgacag     420
ttttctgtt tccggagag ccagttgata ttgcagtcag tgttcacagg acaatgcagg     480
aattgtatac ctgcagcaaac gaaacagaaa ttcccggtaa ctgttaccg gtcgataaag     540
ttattcaa ggataatatc gaaatcccgg caggtcttta aacagttccg taataaataa     600
```

<210> 424
<211> 1
<212> DNA
<213> Escherichia coli

<400> 424
```
cgatccacc aagaagatgc ggttgtaccg tcatcaacca gatgcgcaaa gctactcagc      60
aactacct tcttcgcaat aagcacgcca ttagcgtcat                            100
```

<210> 425

<211> 465
<212> DNA
<213> Escherichia coli

<400> 426
tcgcgtgttt accttcaaca tcggtaactt tctggcggat agtttcacgg taagcaacct   60
gcggtttacc tacgttcgct tcaacgttga attcacgctt catacggtca acgatgatgt   120
cgaggtgcag ttgcccata cccggatga tggtctggtt agatccttcg tcagtccata   180
cagcgaaaaa cgggtcttct ttagccagac ggcccagagc cagaccattt ttttcctggt   240
cagcttgct ttcggttca actgcgatgg agattaccgg ccaggggaat tccatacgtt   300
tcagaatgat cgccgcatcc gggtcacaca gggcgtcacc agtggtacg tcttcagac   360
ggatagcag aggatgtcg cccgccgaa cttccttgat ctcttcacgt tcgttagcgt   420
tcatctgaac gatacgaccg aaacgctcac gtgcagcttt cacgg   465

<210> 427
<211> 653
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(653)
<223> n = A,T,C or G

<400> 427
ngatcggctc aagcagaact ggtttcgctt tcttaaagcc ttctttaaag gcgatagaag   60
tacttacttt aaacgccagt tcagaggagt caacgtcatg gtaagaaccg aagtgcagac   120
gaatacccat gtctactacc gggtacgctg ccagcggacc tgctttcagc tgttcctgga   180
taccttatc aaggtcgggg atgcattcgc caggattac accacctta atgtcgttga   240
ttaactgta gcctttcggg ttgaacccg gctccagcgg gtacatgtcg ataacaacat   300
tacatcaccg accagacca ccagactgtt tcgcgtgttt accttcaaca tcggtaactt   360
tctggcggat agtttcacgg taagcaacct gcggtttacc tacgttcgct tcaacgttga   420
attcacgctt catacggtca acgatgatgt cgaggtgcag ttgcccatac ccggatgat   480
ggtctggtag attccttgtc agtccataca cggnaagacg ggtccttttt agccagacgg   540
tccagacca gacccatttt tttctggcag ctttggnttc ggtcaactgc gatggaaata   600
ccggagcaca ggaattcata cgttccanaa tgatcggggc attccgggtc aca   653

<210> 428
<211> 264
<212> DNA
<213> Escherichia coli

<400> 428
ctttcttaaa gccttcttta aaggcgatag aagcagccag tttaaacgcc agttcagagg   60
agtcaacgtc atggtaagaa ccgaagtgca gacgaatacc catgtctact acgggtagc   120
tgctgcaccg acctgcttc agctgttcct ggataccttt atcaacggcc gggatgtatt   180
cgccaggat cacaccacct taatgtcgt tgatgaactc gtagcctttc gggtttgaac   240
ccggctccag cgggtacatg tcgataac   264

<210> 429
<211> 200
<212> DNA
<213> Escherichia coli

<400> 428
gttttgcgga gatgtaaggg ctaatctgaa tggctgcatt ccttgtttaa ggaaaaacga   60
atgactcatt gccgatacct gattaaacgg gtcatcaaaa tcatcattgc tgttttacag   120

```
ctgatccttc tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt   180
cggacgcacc tttaataact ataaataagt gtctgggcag atactatata aattaactta   240
gtgaatgatt atgctaatgt catcaattaa ataaatataa tggcgttaag gcttcccagt   300
aatataatta atactctact tccagagtag                                     330
```

<210> 429
<211> 465
<212> DNA
<213> Escherichia coli

<400> 429
```
attttgggga gatgtaaggg ctaatctgaa tggctgcatt ccttgtttaa ggaaaaacga    60
angactgatt gccgatacct gattaaacgg gtcatcaaaa tcatcattgc tgttttacag   120
ctgatccttc tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt   180
cggacgcacc tttaataact ataaataagt gtctgggcag atactatata aattaactta   240
gtgaatgatt atgctaatgt catcaattaa ataaatataa tggcgttaag gcttcccagt   300
aatataatta atactctact tccagagtag aatattaaat tttatccgcg tggtgcatca   360
ttacaaattt atcccacaac tgttccttcg tctcgacatg cgccggatct tccacaatag   420
aattgggat cgggcacacc ttctggcagg ttggtgtctc gtagt                     465
```

<210> 430
<211> 579
<212> DNA
<213> Escherichia coli

<400> 430
```
aactgaatg gctgcattcc ttgtttaagg aaaaacgaat gactgattgc cgatacctga     60
ttaaacgggt catcaaaatc atcattgctg tttacagt gatccttctg ttcttataac     120
ataagaaac gtacttaagg tgcgtccggt gaaccagtcg gacgcacct aataactat     180
aaataatgt ctgggcagat actataaa ttaacttagt gaatgattat gctaatgtca     240
tcaattaat aaatataatg gcgttaaggc ttcccagtaa tataattaat actctacttc     300
cagagtagaa tattaaatt tatccgcgtg gtgcatcagc aaaatttat cccacaactg     360
ttccttcgtc tcgacatgc                                                  579
```

<210> 431
<211> 443
<212> DNA
<213> Escherichia coli

<400> 431
```
aagatgatgt gatgagaaag tcaatttgaa taagacaata ttaagagcta aaaaaatgtc    60
aaaatatact aaatctaaaa atataatggcat tagaaaatat aatgcgaaaa cggaggtgaa   120
anttttat ttaaatgat gaaaatctcc cggcaaaaa acgggagat gaaagtgtga   180
tcggttatcaa ataaacaaca gaggagaaat ttttaacgca gccattcagg caaatcgttt   240
aattcattg cctggcggat aagttgcggc ttaacgccag gaagcgtgtc ggccagttc    300
aaattaatat cacgcagcag ttttttcgcc ggattggtac cggaaaacag atcgcggaat   360
tcctcgatac cagccagcat caacgcgcca ctgtgcttgc ggctacgtc atagcgacgc   420
agataaagt actgccgat gtc                                              443
```

<210> 432
<211> 573
<212> DNA
<213> Escherichia coli

<400> 432
```
caggtggttt gttgtgggca atgatgcatt taagttatcg tctgcagata gaggagatat    60
tacaataaac aacgaatcag ggcatttgat agtcaatacc gcaattctat caggagatat   120
```

agtcactcta agaggaggag aaattaggtt ggtattatag cttgtgcgcg ccatgattgg   180

cggcaattt aaacttagtg ctttacatcg ctattgtctt gatttctttg aattattttta   240

taaattaaaa aaacgactgt tatgtataag caaaggtccg aacgaaaaat acattccaaa   300

taaatgcttg cttaaatctc tatatccttc ccgaaaaat gacacataaa attgagatat   360

tccaaaaaga gatactacaa ataaagatgc ctttatttta ttattctaa taaaaataga   420

agcattaaaa aataataaca atgatataaa tctaatgtt ttaaatatat tgtcttttat   480

gttagtaata gtcgttagta tgtttgatcc tccatatatt acgtgtagtt ttttatatac   540

atggaaataa ttttcttat actgagacat cacaccatca tcaaatggaa gtttgaagat   600

ggtgcctggt ttgctaacca ataaaaagag tgcattcg   638

<110> 433
<111> 249
<112> DNA
<113> Escherichia coli

<400> 425
ctttacttgg catgatccac ttcgccagaa tacggcaat aagcccaaaa ataatccatg   60

acaghatgcc cattgtttcc tcacttatct gttttgcatt agcgggttag tcgctgataa   110

aagtaatacc acaacatcgg gaggcaaga tttgtyacga gcatcacgga ggtttttttg   160

cgatcgcgca gaaattgggc catcaacgat cagtgataat tacccaaccac aaacatcatg   240

ttcgtttttcc gtgtcataag aacgtacggt attcaccaga tcttttatca cttcagccg   299

<110> 434
<111> 299
<112> DNA
<113> Escherichia coli

<400> 434
caaaaataag cgaatatcgg gtaaaggcat cagcccgacg aatacgtcgg gctacaaata   60

ttattgtct gcaggtgtt tagcgggtg ttgatccaca ggttctaact ggaagacac   110

atcgacttga tcatcaaat gaatagcggc ctgctcgtaa gttcctggg cggacacgg   160

cgtcgcatcg gctttcatca tccgcaccat tgggctgggc tgatagttgg aaacatggta   241

ccgcacatta tataccggcc ccagtttacg atgaagccg ttcgccagtt cctcgcgctg   319

atgaatccg ttatcaatcg ctgcttacg cgcttgtct ttataggcat ccggctgcgc   379

tacccgacc gacacagaac gaattccc   388

<110> 435
<111> 381
<112> DNA
<113> Escherichia coli

<400> 435
ctatccttga tgaaaccgcg agcaaagata ggtgattacg tcatggtttt acagaaaatt   60

ctagaaaag gaggcaatat cgggtaaagg cattagcccg acgaatacgt cgggctacaa   170

ctattatgt gctgcaggtg ttttagcggg tcgttgatcc acaggttcta actggaagac   180

tccatccacc tgatcatcaa actgaatagc ggcctgctcg taagttcct gggcggacac   240

cggcgccgca tcggctttca tcatccgcac cattggctgg gctgatagt tggaaacatg   300

gtacccgacc ctatataccg gccccagttt acgatgaaag ccgttcgcca g   351

<110> 436
<111> 762
<112> DNA
<113> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(762)

<223> n = A,T,C or G

<400> 436
aattatgaaa cactgtctgg aatcgtctga atgacgggca catttgcgag cacgcatcca 60
gtaataacac aggaaactat tttatctacg cgttagcgat agactgcttg catggcgaaa 120
ttagttaatc cgacgatttc agcgggacgc tgaaacggga aagcccctcc cgaggaaggg 180
gtcataaata aggaaagggt catgatgaag ctactcatca tcgtggtgct cttagtcata 240
agcttccccg cttactaaga ctaccagggc ggggggaaac ccgtcctacc ctcactcctg 300
aaagtatgcc ttaacgataa gatcgtcaat ccgcaggctt tgtagtctgc gatcctgcca 360
gaaaatattc tttgcgagtc gttacgcaat aatcacagag gaaactattt tattcacgcg 420
ttagcgatag actgcattca gggcgaaagg aggtaagccg atgattcag cgggacgctg 480
aaacgggaaa gccctcccg gagaagaggg ctttaataa ggaaagggtt atgatgaagc 540
tactgtgata ctcttagtga ttagttttca gggttactaa gaacaccagg 600
ttgtaggggg aacctctcc taaccctac ttctgaaatt gggtgctatg acgctggcgt 660
tactccttan cgtaccagt ttgtctgcc tggcgttgt aacgccagat cggtaccgt 720
ttgaatattt taatgaaagc cgacaaatca atcacgtga cg 762

<213> 457
<211> 290
<212> DNA
<213> Escherichia coli

<400> 457
tccatctgcg agcacgcatc cagtaataac acaggaaact attttatcta cgcgttagcg 60
ttagctgtct tgcatggcga aaggaggtaa gccgacgatt tcagcgggac gctgaaacgg 120
gaaagccctc ccgaggaaag gggccataaa taaggaaagg gtcatgatga agtactcat 180
catcgtgctg ctcttagtca taagcttccc cgcttactaa gactaccagg cggggggaaa 240
cccgtccttca ccctcactcc tgaaagtatg ccttcacgat aagattgtca at 292

<213> 458
<211> 651
<212> DNA
<213> Escherichia coli

<400> 458
attttagatt tttacgaaat catgggatca ctaacaaat atcgcttgtc agttatattg 60
tatcgcagaa aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 120
ttaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tgggccgcac 180
cagccacgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 240
ttgctgactt taagcattc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 300
tttttaaaat taagcagtgg cagttgcgta accgtgccgc gcctgatgcc gggacgcact 360
ttactctatct gggtggcgcg cacgtgctga tcagcgacac cgacggtaaa atcattaaag 420
cctacgacgg ttagattttt tatcatcgct aaaaaagcc ccctcatcat gaggggaaa 480
tggacatatc ttgttatttt ttattattag ccactgctc gtcttgcttg ttattagtcg 540
tatttcaaat tgattaatgc ggttgcctcc agtgcgccag atttaacttt gttttgtatcg 600
tagacgtagt aactggctgt tatcggaatt g 631

<213> 459
<211> 606
<212> DNA
<213> Escherichia coli

<400> 459
tatgccagca aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 60
ttaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgccgcc tgggccgcac 120
cagccacgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 180
ttgctgactt taagcattc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 240

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agtacaacat taagcagtgg cagttggta acctgcccgc gcctgatgcc gggacgcact   300
ggacctatat gggtggcgg tacgtgttga tcagcgacac cgacggtaaa atcattaaag   360
cctagcacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa   420
ttcagacacc ctgttatttt ttattattag ccacttgctc gtcttgcctg ttattagtcg   480
tatttcacgt tgattaatgc ggtgcctcc agtgcgccag atttaacttt gtttgtatcg   540
tagacgtagt aactggctgt atcgaa   566

<110> 440
<111> 939
<112> DNA
<113> Escherichia coli

<400> 440
catatttaca tcctttgat tggtgataac atgcgaatcg gtattatttt tccggttgta   60
atcttcatta cagcggtcgt atttttagca tggttttta ttggcggcta tgctgcccg   120
tagtataaa gatgaaaaaa acaacgatta ctatgatggg tgtggcgatt attgtcgtac   180
tcggcactga gctgggatgg tggtaacgtc acctctaaaa aatagcaaag gctgcctgtg   240
tcgagcttt gggcaattta agcgttaact tttaatcctc ctgtagataa atagcacgac   300
aatctcacca ataacggaa ccacgaagct gccaaaatt   339

<110> 441
<111> 576
<112> DNA
<113> Escherichia coli

<400> 441
catgtatatt taaaaaggaa aacgacatga aacgaagca cagaatcaac attctccaat   60
catcaaatat ttccgtggag catcttatta ttgaatatag aggtttaact ccggtaaaaa   120
ataaagctca attgaatgca gggaaaaata atatggccat aaaaaacatc gaaagaaact   180
tcttttagttt aacatgtaaa cgcatggtta atcctcatat caggggtgga gtgttaagaa   240
catatataaa tggagcatg tttccctt tcattttatc aagttcctgt tgccgttta   300
tccatcttct aattgcatat ttaattttt ctgataaatg gcattgagca tcgatttcat   360
ttaaaacatc tgtaca   376

<110> 442
<111> 446
<112> DNA
<113> Escherichia coli

<400> 442
ttaccatagc tattagtaaa aatataagag ttagctgtat tgttatgtct gtggcgaaat   60
tcactacctc cgttttttg attaagaatg attttattat cgtaagtaaa attacatgaa   120
tcttttaaaaa ggaaaacgac atgaaacga agcacagaat cascattctc caatcataaa   180
tattccgt ggagcattct attattgaat atagaggttt aactccggta aaaaacaaag   240
aagcattgaa tgcagggaaa aataatatgg ccataaaaaa catcgaaaga aactcttta   300
atttaacatg taaacgcatg gttaatcctc atatcacggg tggagtgtta agaacataca   360
taaatgcatt catgttttc cttttccatt tatcaagttc ctgttgccgt tttagtccat   420
tctaattgc atatttaat ttttct   446

<110> 443
<111> 343
<112> DNA
<113> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(383)

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<223> n = A,T,C or G

<400> 443
tgaacccggt gccgattttc aggcatcctg atttaactta gcacccgcaa cttaactaca   60
gtaaaacaaa gagataaatg tctaatcctg atgcaaatcg agccgatttt ttaatcttta   120
cggattttta cccgcctggt ttattaattg cactgtnatc cgggcgttcg cccgctttaa   180
tgacaatagg ctgtgtagcc tgggcctgtt tctctttcac ccggcgcaga gggcagcaa   240
ttcgcatcttt atccttggct gcaggttgaa cggctgcgct cttatgtcgt tcaaggcgag   300
tcggttttttc gggctccaga cgagcctggc gcgcttcgaa acggcgtttg gcttctgggg   360
cacgcttttc ttcctgacga atagccgc   388

<210> 444
<211> 209
<212> DNA
<213> Escherichia coli

<400> 444
aattttaata acgctatctg cggataaaagc agaataggtg gttaacccca gacataaacc   60
cagcaaaata atgttattgt atttcataat ctattgttcc ttagcgacag attgctgtct   120
cgtcttttcag taaggtacca ggagaaaactt caggaagctc gtactcgaca atacagtttg   180
cgtttttatc cttgcccbat gaaacctgt   209

<210> 445
<211> 341
<212> DNA
<213> Escherichia coli

<400> 445
tatctttaat acggttaaat gcaacccgaa cccccgttgt ccctttgctg cattcactta   60
cagttattcg aaaagggacg gctggacttg tgctacccgt cgtcggaaat tgtctggcac   120
tgttttttg gagatctacg gtaaaattaa gcggaatcga tgagactgtg cagccataat   180
cgaccatgcg cccgctaatt ttaataacgc tatctgggga aaagcagaa taggtggtta   241
atgccagaca taaacccagg aaaataatgt tattgtattt cataatctat tgttccttag   300
ttatcgattg ctgtctgctg gttcagtaag gtaccaggag a   341

<210> 446
<211> 697
<212> DNA
<213> Escherichia coli

<400> 446
atattttactg ccaatttccg gcgagatcgga aagggttaam ccatattgat ccataaaggt   61
atgaatccg ggctatacg ccaggcatgg cttgagccat ggcattaaat tcggcaaatt   120
cgggcgnttga ttcttccgac gcggttattc tggcatacac cagatccagc aagggggtttt   180
taggatcgtt gagcagcaga tgatctacca gttccagcgc ctgggtgtat tgttcctcgt   240
ttcgaataccc cgcagaaaa ggtgccacag cagttagcct ttctccgct tgcaagatgt   300
tggcaatcgc aatcattttt tcccttagt acgatgaaca gcgctaaaga aatcgtattc   360
tttatcgcgtc ataacttcac gtatgtagca cttttgcgat tcaaaaaga ccattgctac   420
aacaagtaat tcattgcccc caacattgaa aacataatgc ttatccagat atttgaagtt   463
atccagagat gggaatactg cttttaatga ctcaggtttt ttgaaatatc ccttagcaat   541
tgtgatccc agagccacca actccgtttt atgttgcggg tattttccg cagcatcttt   600
caaatccttt tgagttatca ggtgcattct tcatcacgtc cgtkgmcaaa ttggcaatat   660
aataacatcc gttgccagat tggcacggat gaattat   697

<210> 447
<211> 213
<212> DNA

<213> Escherichia coli

<400> 447
aattaataac ttttcgttag gcagtttttgg gtgtgagttg caagagggga gactactgaa   60
taaatcaagt tttataatcg aggggaaaat ggtgatggcg ttcatagcaa aacgccctca   120
aacataaagg tcgagggcgc ttaagatgtt aaaaaccgc tatccgttaa aaaacaatgt   180
tcaactaagg tcagtgacat tgcgctaaaa aagcg   215

<211> 448
<211> 345
<212> DNA
<213> Escherichia coli

<400> 448
gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac cattgttat   60
ttaacgttca attatctgtg tgtgatattt tattgaatgt tttaaatatt gttttattg   120
tcattgtat aaatattggtt atcattgct gaatggattc agtcttaatg agtgggtttt   180
taaacgacag gcatagagta atgatacgta tgcataacca acatctttac tcattatgtc   240
attgaatgtt gacgctatc ggttatgagg gagaggtatt ttcagttgat ctggattgtt   300
taattcatat aatgcgcctt tgctcatgaa tggatgccag tatgtagtgg gaaattataa   360
atattgaaat agtccaacta cttcttatt accaa   395

<211> 449
<211> 641
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(641)
<223> n = A,T,C or G

<400> 449
ataatcaggt aagaaaaggt gcgcggagat taccgtgtgt tgcgatatat ttttagttt   60
ngcgtggcaa tacatcagtg gcaataaaac gacatatcca gaaaaatata cactaagtga   120
atatatctt ccgatttatc ttaatcgttt atggataaag gcaaagggt tcgtttttc   180
tacacttat tcagcactca caaataaagg aagccaatg aaaattatac tctgggctgt   240
attcattatt ttcctgattg ggctactggt ggtgactggc gtatttaaga tgatatttta   300
aaattaatta atgtcatcag gtccgaaaat aacgagaata tttcagtctc tcatcctgtt   360
ttcacttcgt catgtgcatt ggttcatata atcactggcg caaggagcg cgcaggcgna   420
natcgacagn cgnccacct naccccatgc cgaacttcag aantgaaaac nccntaacnc   480
nggnngtcgg cgggngcctc cccatgcnan agtangggaa ntgccangcg ncnnattaaa   540
ncgaaggctn attncaaaga ctgggccttn cntttatctg atgtttgtcg gagaacgctc   600
nctcgagnan gacaaatncc gccgggagcg gatttgaacn t   641

<211> 450
<211> 314
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(314)
<223> n = A,T,C or G

<400> 450
gaactacgag taagaatagc tncgaattcc cgtttatgga taacggcaaa gggcttcgtt   60

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```
ttttcctata cttattcagc actcacaaat aaaggaacgc caatgaaaat tatactctgg    120
gctgtattga ttattttcct gattgggcta ctggtggtga ctggcgtatt taagatgata    180
ttttaaaatt aattaatgtc atcaggtccg aaaataacga gaatatttca gtcctctatc    240
ctgttgcgct cctgtcatgt gcattgcttc atataatcac tggcgcaagg agcgcgcagg    300
gggntntnnt cttt                                                      314
```

```
<210> 451
<211> 336
<212> DNA
<213> Escherichia coli
```

```
<400> 451
atatacacta agtgaatgat atcttccgat ttatcttaat cgtttatgga caaaggcaaa     60
gggcttcgt tttttcctata cttattcagc actcacaaat aaaggaacgc caatgaaaat    120
tatactctgg gctgtattga ttattttcct gattgggcta ctggtggtga ctggcgtatt    180
taagatgata ttttaaaatt aattaatgtc atcaggtccg aaaataacga gaatat        226
```

```
<210> 452
<211> 414
<212> DNA
<213> Escherichia coli
```

```
<400> 452
ttgaaattac cgtgtgttgc gatatatttt ttagtttcgc gtggcaatac atcagtggca     60
ataaaagtc atatccagaa aaaatatcac taagtgaatg atatcttccg atttatctta    120
atcctatg gataacggaa aagggcttcg ttttttccta tacttattca gcactcacaa     180
ataaaggaac gccaatgaaa attatactct gggctgtatt gatatttttc ctgattgggc    240
tactggtggt gactggcgta tttaagatga tattttaaaa ttaattaatg tcatcaggtc    300
cgaaaataac gagaatattt cagtcctctc atcctgttgc gctcctgtcat gtgcattgct    360
tcatataatc actggcgcaa ggagcgcgca ggggggcggcc aatcgccgcc gcccctg       414
```

```
<210> 453
<211> 531
<212> DNA
<213> Escherichia coli
```

```
<400> 453
aacaatttgc ccatgcgctc ggtcatgcgc tgcatcgccg ggccatttg gcggtcccg      60
cgacgcat tcgactgtta atggcgaat cttcagtact ggtattagt ggacaacgcg       120
cgtcctaa acggctggaa gaagcgggtt ttgcgtttcg ctggtacgat ttagaagagg      180
ctctcgga tgtcgttcgc tgatgtggct taaagcaaac atcggccagt taactcccgg     240
tgttacagga ttagtggctt tgcgcgataa gatcgtctgg tgaaagtcgg gtcaccatca    300
taacaaatc tctgtctaaa cctctatcca gcatctcctg agcaatacgc agggcttctt     360
ctgtcttgcc ctgcattgcg cctttttcac gtaatctgtc agcaatggtc atcaagtttc    420
tctttttctt gtggtgcgcg ttccgctatc tcaccaataa atgcacgaaa acgctgggca    480
tccctgttt gtaatacgta attaaacagg gctttagct gtctgtgatt agtgktcctc     531
gtaactagca g                                                         541
```

```
<210> 454
<211> 95
<212> DNA
<213> Escherichia coli
```

```
<400> 454
tggcatctcg gtgttgccga tcttcatgat atccagcccg ccggaaactt cttccaaac     60
ggttttgctg ttatccattg agtcacggaa ctg                                  95
```

cggccatatg aacggcgggt taaaatattt acaacttagc aa 242

<210> 450
<211> 300
<212> DNA
<213> Escherichia coli

<400> 450
ttgtggttcc ggtaaaaggt gcaaatgctc aggacgttgc agcgttttgc gtgaccgctc 60
ctggaaggca aaaattgcctc tgggaaagca ttgcgcgggg tccggcgctc atcaacaatc 120
gggtgtgac aaggggctga aacgggaaag cccctcccga agaaggggcc ttgtataagg 180
aaaggttat gatgaagctc gtcatcatac tggttgtgtc gttactgtta agtttcccga 240
cttactaaca actcatcaga gggggagaa atcctccctt acccttgttc ctttactcta 300

<210> 460
<211> 245
<212> DNA
<213> Escherichia coli

<400> 460
tcccgggtgg cggctcatcaa caatcgggggg gcagcaaggg gctgaaaggg gaaagccct 60
ttgcaaacag gggccttgta taaggaaagg gttatgatga agctcgtcat catactggtt 120
gtgtgttac tgttaagttt cccgaccacc taacaactca tcagagggggg gagaaaatcc 180
tccttattc tgttcctta cctctaggttg aaaaaaacaca aggtcaata ggcctgccat 240
ttaaaaacg agatctgtga aacggttttcc ggttagtcctt ttttatcctg ttg 295

<210> 461
<211> 539
<212> DNA
<213> Escherichia coli

<400> 461
aaatacagga ggctgggaat gcgccagaaa tatagattac ttttcttaat agtgatttgt 60
ttctggttt tattttttac ctggacgata agagattcac tgtgtgaatt gcatattaaa 120
caggagactt atgagctggc gggcgtcttta ggctgcaaat tgaaagagta agagtcttcg 180
tgggttaatt attcccgcct tacttacggc gttgggcatt ctcattgcac ccaaatttat 240
tttttacttaa aataataata gatttttta cggatcgat tattttattc ctgaaaacaa 300
atattatat ccccgcccca tggcagggat cttagattct gtgctttcaa gcagagatt 539

<210> 462
<211> 675
<212> DNA
<213> Escherichia coli

<400> 462
ttaaacaatg tcctgacctg ggttcggggg acaacaaaac gtgccgagat gatcctgtaa 60
ctattatcag ttgtgaagta gtgattcacg acttcaaggc gcttttcaaa agggtatttt 120
ggcttcgaca tattaggggc tattccatt catcgtccaa caaaatggt gcagtacata 180
ctcgttgac atcaacacag gaggctggga atgccgcaga aatatagatt acttttcttta 240
atatgatt gtttcacgct tttattttc acctggatga taagagattc actgtgtgaa 300
ttgcatatta aacaggagag ttatgagctg gcgggcgtttt tagcctgcaa attgaaagag 360
taagtgtctt cggcgggaaa ttattcccgc cttacttacg gcgttgggca ttctcattgc 420
acccaaatttc attcttcaca aaaataataa tagatttttat tacgcgatcg attattatt 480
tcctgaaaac aaatataaaaa atccccgcca aatggcaggg atcttagatt ctgtgctttt 540
aagcagagaa tacaggcggg ttacgttacc agctgccggg ccttagcgc cgctttcgat 600
ggtgaaggac actttctgac cttcgtccag agatttgtaa ccatcgttct ggatagcaga 660
gaagtgtacg aac 675

<210> 463
<211> 629
<212> DNA
<213> Escherichia coli

<400> 463
tagtggcatt ggttgctgga gagagaaaac ccccgcacgt tgcaggtatg cacctgacaa   60
taccacgttg gctaatcttg actctagacc actaagaat agccgcgaaa cgttgtcatt   120
ccaacacagg cggctatatg acgttcgcag agctgggcat ggccttctgg catgatttag   180
agctccgtt cattgctggc atccttgcca gtatgatcgt gaactggctg aacaagcgga   240
agtaacgtgt catgcgggcg tcaggctgcc gtaatggcaa tttgcgcccg gaccaggccg   300
tagggggtaa actctgcggc cttttcgtt cctactgcgg gtaaggcacc cagtcgccgc   360
tgttcagttg aacgtacggt ttatcctggt attgaataac tactgcattt gagttctcgg   420
agacaggtcc tgttgtgggc aaaccactgg tgagtttttt ccagtcaaca ttgcttcgg   460
tgaaaatctt gccatcgaga acgcgaacca ccagatcgga gatagccagg aagctgctcg   540
ctgttcgat gacaatcggc gcccctgat gcggttgctt catgccgaag aatttcaccc   600
taacgcggac gtcggtgata gacgggctag   630

<210> 464
<211> 541
<212> DNA
<213> Escherichia coli

<400> 464
atcaggctcc tgattgtctt tttgtgcaat ggcgcggtat tagcgtcgtt gctgtcgatg   60
tagtaatca caaacgtggt gaatgatgat tgttagcaag gaaaactgtc aaaaatcttc   120
taagaatttg agggataagg ccggaatggc tccggccaga gggaagttaa ccgcgaagct   180
atcgtctttt gagggtgtt ctaaccagac gccaggcgct ccatacgcca aaaccgcgtc   240
tagtccacg gaccagcata tcaggatggc gaatcgtcca gatcgccatc agctactgc   300
taatcagtgc ccaggagcgc agacttagca gcatattcca gcgacgatcg taagcgcctg   360
ttgtgtccag ccattcacga cgactggcgg a   391

<210> 465
<211> 625
<212> DNA
<213> Escherichia coli

<400> 465
atctacgac accataaaag gaggcaaata atgctgggta atatgaatgt tttaatggcc   60
gcatggaaa caatttcatt ttctggtttt ctggccgcgt atttcagcca caaatgggat   120
gactaatgaa cggagataat ccctcaacca acggcgccct tgctacagtt gtgtacaagg   180
gcccttgatt ttatgacggc gaaaaaaaac cgccagtaaa ccggcggtga atgcctgcat   240
ggatagatt gcgtttcgct tttacgctaa caggcattt cctgcactga taacgaatcg   300
ttgacacagt agcatcagtt ttctcaatga atgttaaacg gagcttaaac tcggttaatc   360
acattttctt cgtcaataaa catgcagcga tttcttcggg tttgcttacc ctcatacatt   420
tcccggttcg ctcttccaat gaccacatcc agaggctctt caggaaatgc gcgactcaca   480
cctgtcttca cggtaatgtt gatatgcct tcagaatgtg tgatggcatg gttatcgact   540
aactggcaaa ttctgacaca tgcagacat ggttcttcat cattagccgc tttgacaata   600
tcgataaatt cttcgccccc gtagc   625

<210> 466
<211> 6.3
<212> DNA
<213> Escherichia coli

<400> 466

tgcttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca   60
aaaacgataa tctgaaagag ccaaggtatt tcagtataag cattgaatgc gacagtaaac   120
tccttggta tcagccagag agtgagacca aaaatgataa tcgtatacat aagtctttcg   1??
a?tggctcgt tagcaaaaag tttcaacaat ggagtaaaata catccaacat atcaataact   2??
ctcatcgta aggtattga aatgttaaca caagctctcg ctgtaggggt atagccgaga   ???
caacgatgc cggaggttgg tgaaataaaa cgggcacaa cacgaaggcg cattt?cgat   ???
a?ccataag agtcggtcgg gtctgttaaa tttaaatggt gggagtgcgc ctccggttgt   400
aaataacac attgctgtc gtagcctgg cggcatcagt ttttttcttg aagtcgggt   4??
gtgtcgcc cctttaaag tgaattttgt gatgcggtga atgcggctaa gcgcacgtgg   ???
caccgttata agtcatgta gtcctattg gtttgggtgg gaaagccgac tgtaattgtt   ???
a?ctgttgc agtcacctgg agg   ???

<210> 4??
<211> ???
<212> DNA
<213> Escherichia coli

<400> 4??
tatttacta aaagagattc atctttgtat aaataaagat aagtaattac gcataaaaca   60
ctaatgatta taatagcaaa aataaatatt atcatctttg atagattact tgagatagcc   1??
gtcatcttgt aaagcctta tcgtttttt atgtctgga ttaatataat cactacatct   160
atctaactaa tctgctgttg atggacatgt caaccatgg tcatttacag ccaa   1?4

<210> 4??
<211> ???
<212> DNA
<213> Escherichia coli

<400> 4??
attacctatt tcggctaaaa tagagactac atgtcttcgg tccatctcac ttaaggagtg   60
t?gttccctt gtaagttttt tcatagcttg cactgctaaa tttcgaacaa ggaatttcct   1??
gtc?ctaatc tctaaaaaga tgggcatggt tacaatgatt tctgctcct ttgattact   1??
at?gaccat gtccatgatt tcgtttaaga atgaagagaa atcactaaac gaactgaata   ???
tattc?cgt gccaatatta tctctaattt caaaaaagtt actttaatg tcggtaatga   ???
??cccaacta ttgatagtgt cttatgtca gataatgccc gatgacttg tcatgcagct   ???
c?aacgattt tgagaacgac aggacttcc gtcccagccg tgccaggtgc tgcctcagat   ???
t?aagttatg ccgctcaatt cgctgcgtat atcgctttt cttatcagt cgttgatgtc   ???
a?tcgttttg accacgagg agcttcacgc gagttcttga aaacctga   ???

<210> ???
<211> ???
<212> DNA
<213> Escherichia coli

<400> 4??
caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga   60
aattaatcca attatcgaaa attcaaaaaa tatccaaaaa tagtatactt tattccagaa   1??
gagttcaata caatgtttgt cttcaatttt tcttacttca gggtaatata gattgctcat   1??
tacattgtga gcttcatctt tatttaattt tctgttgact ccagctctcc gtgataacgg   ???
ttctataatt agatgcttat c   2??

<210> 4??
<211> ??
<212> DNA
<213> Escherichia coli

<400> 470

```
agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcaccc ttaccctgct        60
ctttacgtac ttctgcgttg atagtaaaca tttctttc                                 98
```

<210> 471
<211> 259
<212> DNA
<213> Escherichia coli

<400> 471
```
agcgcgaccg aagtcgatgt gctgcagctt cggtttgtac gggtgacgct gtacgtcctg        60
agctttaact ttgatttctt tacgtcaac aaagatggtc agaacttcgc tgtagaattc        120
agctttagct tgatgttca tgactttgtc gtgatccagc tcgatagcca gcggcgcttc        180
tttgccacg tagatgattg ccgggaactt gttagcggca cgcaggcggc ggctcgcacc        240
cttaccctgc tctttacgt                                                     259
```

<210> 472
<211> 94
<212> DNA
<213> Escherichia coli

<400> 472
```
aaaaacggcg taaagaaagg atgcaaacat gttaataaaa actcaaattg atcccacgta        60
tatattactc cgcaaaatcc ttacaataaa cagg                                    94
```

<210> 473
<211> 174
<212> DNA
<213> Escherichia coli

<400> 473
```
ttacttatta aaatagtgta acgcgattat gtggttatgg cggtaaacat taaataaacc        60
atcgggaagg ggagtaaag tgaaaaaata aaaagcggat aatcttaata agcaggcgg        120
atacaatgc catcggcac tgataagagg ttatttcag ctcatcaaac atcg              174
```

<210> 474
<211> 156
<212> DNA
<213> Escherichia coli

<400> 474
```
ctgtaaaaac gtcaaaaaga gtgtttatc aacagaagaa tggaggtctg acagatagta        60
gtaatgtaaa aaaatggaga cttaagttga atgaacggga gtaaagcgaa aagactatag       120
aagtaaagag aaattccc                                                      156
```

<210> 475
<211> 191
<212> DNA
<213> Escherichia coli

<400> 475
```
tttgttggct taatattcta ttgttatctt tatttataga tgtttatatt gcatgaggt        60
ctttttggag agaagaatga ggaagatgcg tcgagccaca gaaacgttag cttacatat       120
aacgagggtg atgtgaaatt aatttacaat agaaataatt tacatatcaa acagttagat      180
gtttttgtc g                                                              191
```

<210> 476
<211> 245
```

<400> 476
cggccattta tacaggaaaa gcctatgtca gaacgtaaaa actcaaaatc acgccgtaat    60
ttcctcgtta aatgttcctg cccaaactgc acccaagagt cagaacacag ttttttcaaga   120
gtacaaaaag gtgccttttt gatctgcct  cattgcaaca aagtattcca gacaaatctt    180
aaagctctag cctgattgat tttattagta acaagtattt tttatatttt aataatatat    240
ttaaa                                                                 245

<400> 477
aaattctcag gtaccttgtc accatacttt ttttctgag  cattaatgat attttgagct    60
tcttgatgat ctttaactcc ccacatttgg tggaaagtat tcatattaaa aggaaggttg   120
aatcatttgt ctttataaat cgccagtgga gaattagtaa aacgattaaa ttctactaaa   180
ttattaaagt aatcccatat atatttatca ttggtatgaa aaatatgtgc accatattta   240
ttaatctgga tacctcaca  gtcctctgtg tacgcatttc cacgatatg  atttcttttc   300
ttaatcccta aaacttttt                                                 319

<400> 478
gaagtgatg  aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga    60
tgaatttgc  cggagtcag  gcggcgactt cggtgcggtt acgtccggct ttcttgctt    120
tgttaaatgc caaatctgcc gattttcaac                                     149

<400> 479
gaaagtattt ttggttattga catcactgga aaatataact tgcttttcat tattaaactc    60
gaagtcgta  ccgtatcttg acaaaacattt atcgagctta ccaaatcctt gaagaggttt   120
aactactcat aacatttgcg cgtccttgc  agtaatgccc gtcaaatcct tgaacgggcat   180
tattttacatt aaaattaccag tattttcctcg gagtgaagaa tattaccagg tatatttaac   240
accacgttc  ggggaccagt cttgatctac gtcaccacca ccgaggtagt tagcatcggt   300
ataggcacttg aagttcttgg tgaagctaaa                                     330

<400> 480
tttttttttcca gcaacggagc aaaaggtttg ccctggtgca gctcaggtt  aaccactta    60
actaagtggc gacgacccgg agatgtcggt ttacattaa  caactgccat tgtattactc   120
ctcgacttta ctcagcgcg  ccaacgaagt ccagattctg gccttcttc  agggtgacgt    180
aagctttttt c                                                         191

<210> 491
<211> 14?
<212> DNA
<213> Escherichia coli

<400> 491
tncttttaac tancagggtg ttaacgactt cgacttcgac ttcaaacagt ttctgcacag     60
cagntttaac ttctgctttg gtcgcgtctt tagcaacttt gagtacgatg gtgttggatt    120
tnttcatcgc agtagacgct tttcagaaa cgtgcggtgc acgcagcacc ttcagcagac     160
gtcttca                                                               165

<210> 49?
<211> 1??
<212> DNA
<213> Escherichia coli

<400> 49?
naangcgtta caaagcctgt gaagcccgaa ggctccacag acagtgctac ttgaaggcct     60
tactcttttct tcttaggagc gagcaccatg atcatctggc ggccttcgat cttcgttggg    120
aagnattcga ccactgccag ttcttgcaaa tcgtctttca cgcgattaag ca            172

<210> 4??
<211> 266
<212> DNA
<213> Escherichia coli

<400> 4??
tngtcatttc gggtgattga taaagcaatc atcgttctag gggcgttaat tgcgctgctg     ??
naantgatcc gctttctgct tcagcttctg aactgatagc ggaaacgtaa ttaagggcta    1??
acacacatct actcttagcc ctttaacatt taagcaattg tcacgaactc ttctgccgcc    1??
gttcggtcaa tggcgacggt atcgtcgaag tcttttttgg ttgccccat cttcagcgcc    240
acccgaacc cctgcaacac ttcgtc                                         266

<210> 4??
<211> ???
<212> DNA
<213> Escherichia coli

<400> 4??
nncaagtagc tgatggtcaa caggatgaga gaaacccaga gacaggttaa tcacattgcc     ??
nttaacractt gcacggtaac ctacaccaac cagctgcagc ttcttagtga agccttcggt    1??
acccacgtta accattgagt tcagcaggc acgcgcggta tcagcctgtg cccaaccgtc    1??
ttcgtaatca tcagcgcgac cgaaggtcag ggtattatct gcatgtttaa cttcaacagc    240
gtcttcgaga gtacgagtc                                                 2??

<210> 4??
<211> 7?
<212> DNA
<213> Escherichia coli

<400> 4??
caggtcggaa cttaccgac aaggaatttc gctacctag gacgttata gttacggccg     66
ccgtttaccg ggg                                                       73